

## **FIGURE 1**

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACCGCGTCCGGGCCGGAGCAGCACGGCGCAGGACCTGGAGCTCCGGCTCGTCTTCCCG  
CAGCGCTACCCGCCATCGCCTGCCGCCGGCCGCGCTGGGGCTCTGCCGCTTGCTG  
CTGCTGCCGCCGCCGGAGGCCAAGAACGCGACGCCCTGCCACCAGGTGCCGGGGCT  
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAACAACTTGGCGGCCGGAAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC  
CTGGAGGGCTGTGCAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATCGAGTGGTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCGACTGTCTGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGAGCAGACA  
GGGCGACGGGTCTGCCGTGCCACATGGGTACCAAGGGCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGAAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCAGCGAGTGTGAAGTGGCTGGGTGCT  
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCAGGCCGAGCCGCCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACAGTGCAGAGTGTGACTCCAGCTGTG  
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG  
AAAAGTGCATAACTCCAGGGAGCTACGTCTGTGTGCTACGGCTGAAGAACAG  
GAAGATGCCGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT  
GCCCTCCCGGAAGACCTGTAATGTGCCGACTTACCCCTAAATTATTAGAAGGATGTCC  
CGTGGAAAATGTGCCCTGAGGATGCCGTCTGCAGTGGACAGCGGGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTGTCCTTAAACAGCTGCATTCTGGTTGTTCTTA  
AACAGACTTGTATTTGATACTGAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAC  
TTGGCCGCCATGGCCAATTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA  
TCACAAATTTCACAAATAAGCATTTCAGCTAGTTGTGGTTGTC  
ATCAATGTATCTTATCATGTCGGATCGGAATTAAATTGCCGCAGCACCATGGCTGAAAT  
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGGAAAGAAC  
AGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T) : 2

MRLPRAALGLPLLLLLPPAPEAAKKPTPCHRCGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG  
NGHCSDGSRQGDGSCRHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCSGLTNRDCGECEVGWLDE  
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLA EKT  
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

## **FIGURE 3**

CAGGTCCAAC TG CAC CT CG GT CT AT CG ATT GA ATT CCC CG GG AT CCT CT AG AG AT CC CTC  
GACCTCGACCCACCGCGTCCGCCAGGCCGGAGGCAGCGGCCAGCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGCATGGCCGGAGGAGCGCCTTC  
CCTGCCGCCGCTCTGGCTCTGGAGCATCCTCTGTGCGCTGGCACTGCAGGGCGAGGC  
CGGGCCGCCGAGGAGGAGACCTGTACCTATGGATCGATGCTCACCAAGGCAAGAGTACTCA  
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTTACACATGAT  
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTCTATGAATTCTCTGCGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCGCTCACAGGCA  
TCAGTTGTTCAAGTTGGTTCCATGTCTTGGAAAACAGGATGGGTGGCAGCATTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAAATGCTATCT  
TCTTAAACATGTCAACAAGCTGAGTGCCCAGCGGGTGGCAAATGGAGGCTTTGTAAT  
GAAAGACGCATCTCGAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG  
TACCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAACTGTGACAAAGCAAACCTGCTCAACCACCTGCTTAATGGAGGGACC  
TGTTCCTACCCGGAAAATGTATTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCACAACCCGTGCAAATGGAGGTAATGCATTGGTAAAAGCAAATGTAAGTGT  
CCAAAGGTTACCAGGGAGACCTCTGTCAAAGCCTGCGAGCCTGGCTGTGGTCACAT  
GGAACCTGCCATGAACCCAAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGCGCCAGCTCAGGAGC  
ACACGCCCTCACTAAAAAGGCCGAGGAGCGGGGGATCCACCTGAATCCAATTACATCTGG  
**TGA**ACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCCTTGTAAACCTTCA  
TGTGTTGAATGTTCAAATAATGTTCACTACACTTAAGAATACTGGCCTGAATTATTAGCT  
TCATTATAAAATCACTGAGCTGATATTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTTCTGTTCACTGCTTGGCAGATTTATATTGTCAATTGA  
TCAGGTTAAAATTTCACTGAGCTGAGGAGATTTCAAAATTACAATGCATTATGGT  
GTCTGGGGCAGGGAACATCAGAAAGGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTCAGTTAATGTTGAAGTTACAGCATTCAAGATTTATTGTCAAGATATTAGAT  
GTTGTTACATTTAAAATTGCTTTAATTAAACTCTCAATAACAAATATTGGCACC  
TTACCATTATTCCAGAGATTCACTGAGGTTAAATTACACTGTGGTAGTGGCATT  
AAACAATATAATATTCTAAACACAATGAAATAGGAAATATAATGTATGAACCTTTGCAT  
TGGCTTGAAGCAATATAATATTGTAAACAAAACACAGCTCTACCTAATAACATT  
ACTGTTGTATGTATAAAATAAGGTGCTGCTTTAGTTTTGGAAAAAAA  
AAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGCTTGGC  
CGCCATGGCCCAACTGTTATTGCAGCTTATAATG

## **FIGURE 4**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKIGKSCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
```

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**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 88-92, 245-249

**Casein kinase II phosphorylation site.**

amino acids 319-323

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## **FIGURE 5**

CGGACGGCGTGGCGTCCGGCGGTGCAGAGCCAGGAGGCCAGGAGGCCAGGAGGCCACCATGTGGCAGTTCCTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGCTGGGCCAGCAGGGCTGCTGGCGCCGG  
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGACGCCAGGGCAGGCTACTGCCAGGA  
GCAGGGACCTGTGCTGCCGCGGCCGTGCCAGCAGACTGTGCCCTGCCACTCTGGGCGCCATCT  
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA  
TCCAGTCTTGGAACGTACTGGACAACGTGAACCGTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGCGCCTCTGGGGCATGACCCCTGGATGAGGGCATTGCTACCGCTGGGACCA  
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATAACAGTGCTGAACCCAGGGGAG  
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAAGTGGCCAACCTGATTGACGCCCTTTGA  
CCAAGGCAACTGTGCAAGGCTCTGGGCTTCTCCACAGCAGCTGTCATCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCCTGTCCGTGCCAGAACCTGCTGTCTTGAC  
ACCCACCAGCAGCAGGGCTGCCCGGTGGCGTCTGATGGTGCCTGGTGGTTCTGCGTCG  
CCGAGGGGTGGTGTGACCACTGCTACCCCTCTCGGGCGTGAAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGACAGCCGAGCCATGGGTGGGGCAAGCGCCAGGCCACTGCC  
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAATGGCCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTCCTATAAAGGGAGGCATCTACAGCCACAGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATAACGCCGATGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTAAATACTGGACTGCCAACTCCTGGGGCC  
CAGCCTGGGCGAGAGGGCCACTTCCGATCGCGCCGTCATGAGTGCACATCGAG  
AGCTTGTGCTGGCGTCTGGGCGCTGGGCGTGGGATGGAGGACATGGGTGATCACTGAGGCTG  
CGGGCACACGCCGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGGAAGAGGCCCAATG  
GGCGGTGACCCAGCCTGCCGACAGAGCCGGCGCAGGCCAGGGCGCTAAT  
CCCGCGCGGGTCTCGCTGACGCAGGCCCTGGGAGCCGGCAGGCAGACTGGCG  
GAGCCCCCAGACCTCCAGTGGGACGGGGCAGGGCTGGCTGGGAAGAGCACAGCTGCAG  
ATCCCAGGCCTCTGGGCCCAACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC  
CCAATACCCACCCCAATCCGTATTCTTTTTTTTAGACAGGGTCTTGCTCCG  
TTGCCCAAGGTGGAGTGCAGTGGCCATCAGGGCTACTGTAACCTCCGACTCCTGGGTTCA  
AGTACCCAGCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC  
TAATTTGTATTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAACT  
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCAAAGTGTGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTTCAGATATTATTTCTTCACTGTTTAAAAA  
TAAAACCAAAAGTATTGATAAAAAAAAAAA

## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
```

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTGGCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTTGACACCCAC  
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCTCGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG  
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

## **FIGURE 8**

GCTGCTTGCCTGTTGATGGCAGGCCTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCATCCGCGCAGTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAACTCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGGGAGCCTGCTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCACCCTGACCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTACACAGATCCGCCTGCAGATGCCCTCCAACCCTCTCTGCTGCTGTTTC  
CATGCCCAGGCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCAGGAAGCCTT  
CCCTGCCACCCTATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGG  
GGACAAGAGTCGACGTGAGTCCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTCGTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCT  
AATAAACACCTGGATAAGCCAAAAAA

## **FIGURE 9**

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT  
DPPADGPSNPLCCCFFHGPAGFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRCQALRRAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

## **FIGURE 10**

CCCCACCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCCAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAGGTACCGGGCGTCGATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC  
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGGAAAGAGCAAAGACTG  
CGTGTTCACGGAGATCGTGCTGGAGAACAACTATAACGGCCTTCCAGAACGCCGGCACGAGG  
GCTGGTTCATGGCCTTCACGCCGGCAGGGCGGCCAGGCTCCGCAGCGCCAGAAC  
CAGCGCGAGGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC  
CGAGAACAGAACAGCTCGAGTTGTGGCTCCGCCACCCGCCAGAACAGCGCACAC  
GGCGGCCCAAGCCCTCACGTAGTCTGGAGGCAGGGGCAGCAGCCCTGGGCCCTCCC  
CACCCCTTCCCTTAATCCAAGGACTGGGCTGGGTGGCGGGAGGGAGCCAGATCCCC  
GAGGGAGGACCTGAGGGCGCGAACGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG  
CCCCAGGGCGGCTGGCACAGTGCCCCCTCCCGACGGTGGCAGGCCCTGGAGAGGAACCT  
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC  
CGCTGAAAGGTCAAGCAGTGAAGGCCTTGCAAGACAACCGTCTGGAGGTGGCTGTCCCTAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCCAGCCCCAAACTCCTCCTGGCTAGACTGTA  
GGAAGGGACTTTGTTGTTGTTCAAGAAAAAGAAAGGGAGAGAGAGGAAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCCACCCCCAACTCCCAGCCC  
CGGAATAAAACCATTTCCTGC

## FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDVFTEIVLE  
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTCATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGGTGTAAAGACCAAGACAGCAGGGAGATTATTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
CATTGATTTGCTGTTATTTTTCTTTCTTTCCCACCACATTGTATTTAT  
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTCT  
GAAGTCTTGGCTTATCATTCCCTGGGGCTCTACTCACAGGTGTCAAACCTCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG  
CCTCTGGGATCCCAGGGCGTAACCGTACTCTACCTCCACAACAAACAAATTAAATAATGC  
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCCCATGAACCTTCCAAGAAATGTCAAGAGTTCTCCATTGCAAGGAAAAC  
AATATTCAAGACCATTCAACGGCTGCTTGCCCCAGCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGCCTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTCCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCAATCCGACATGGCCTCCAGAA  
TCTCACGAGCTGGAGCGTCTATTGTTGACGGGAAACCTCTGACCAACAAGGGTATGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTACGTAATTGCTGTCC  
CACCCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCAAGAT  
AAACCACATTCTTGACAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCA  
ACAACCAACTCGGGATGCTGACTCAAGGGTTTTGATAATCTCCAACTGAAGCAGCTC  
ACTGCTCGGAATAACCCCTGGTTTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAA  
ATATATCCCTCATCTCAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAAGTCCGGG  
GGATGGCGTCAGGAAATTAAATATGAATCTTGTCCCTGCCCACACGACCCCCGGCCTG  
CCTCTTTACCCAGCCCCAAGTACAGCTCTCCGACCCTCAGCCTCCACCCCTCTAT  
TCCAAACCTAGCAGAAGCTACACGCCCTCAAACCTTACACATCGAAACTCCCACGATTC  
CTGACTGGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTATC  
CATTGTAATGATACTCCATTCAAGTCAGCTGGCTCTCTTCAACGTGATGGCATA  
CAAACTCACATGGGTGAAAATGGGCCACAGTTAGTAGGGGGCATCGTTCAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTAGTGCCACTGGATGTTTAACTACCGCGCGGTAGAAGACACCATTGTTCAGAGGC  
CACCAACCATGCCTCTATCTGAACACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT  
GTGCTGGTGGTCTTGTCTAGCGTCTTGTGCTGCATATGCACAAAAAGGGCGCTACACCTC  
CCAGAAGTGGAAATACAACCGGGCGGGCGGAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACCTCCATCTGGAGATGACAGAAACCAAGTTTCAGATCGTCTCTAAATAACGAT  
CAAACCTTAAAGGAGATTCAAGACTGCAGCCATTACACCCAAATGGGGCATTAATTA  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGTCACATAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT  
TTGTCATTGAAACTCTGTAATTATAACGGTGTACTATATAATGGGATTTAAAAAGTG  
CTATCTTCTATTCAAGTTAAATTACAAACAGTTGTAACCTTTGCTTTAAATCTT

## **FIGURE 13**

MGLQTTKWPShGaffLKSwlIISLGLySQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTvLYLHNNQINNAGFPaelHNvQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLDNsISTVGVEDGAFREAIISLKLFLSKNHLSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMARVELNMNLLSCPTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTTSLPTIPDWDRGRERVTPPISERIQLSIHFVND  
TSIQVSWLSSLFTVMAKLTWVKMGSIVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNyRAVEDTICSEATTHASYLNNGNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKDnsILEMTETSFQIVSLNNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

ACTTGGAGCAAGCGCGGCGGGAGACAGAGGCAGAGCTGGGCTCCGTCCGCCACGAGCG  
ATCCCCGAGGAGAGCCGGCCCTCGCGAGGCAGAGGGCGACGAGGAAGACCCGGGTGGCTCGGCCCTGCC  
TCGCTTCCCAGGCGCGGGCTGCAGCCTTGCCCCCTCTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCT  
GCTTCTGCTGATCCTCGGACAGATCGCTCCCTCCCTGCCAGGGCAGGGAGCGGTACAGTGGAGGTCCATCT  
CTAGGGCAGACACGCTCGGACCCACCGCAGACGCCCTCTGGAGAGTTCTGTGAGAACACAAGGGCAGACC  
TGGTTTCATCATGACAGCTCTCGCAGTGTCAACACCATGACTATGCAAAGGTCAAGGAGTTCATGTGGACA  
TCTTGCATTCTGGACATTGGCTCTGATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG  
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCTGCTCAACAGGATGCCACTGTCCACGG  
GCACCATGACTGGCTGGCCATCCAGTATGCCCTGAAACATCGCATCTCAGAACAGGAGAGGGGGCCGGCCCTGA  
GGGAGAATGTGCCACGGGCATAATGATCGACAGATGGGAGACCTCAGGACTCCGTGGCCAGGGTGGCTGCTA  
AGGCACGGGACACGGGCATCTAATCTTGCATTGGTGTGGCCAGGTAGACTTCAACACCTGAAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCTTCTGTGGCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTCC  
AGAAGAAGTTGTGACGGCCACATGTGCAAGCACCTGGAGCATAACTGTGCCACTCTGCACTAACATCCCTG  
GCTCATACGTCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAAGATCCAGGATCTGT  
GTGCCATGGAGGACCAACTGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGTGTGCCAGTGCTACAGTG  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGACTACTGTGCTCAGAAAACCACGGATGTGAAC  
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCAGTGCCATGAGGATTGCTCTTAACCCAGATGAAAAAA  
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGAAAACCTGCAGCCAGTGCTCAGAAGGCTCC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACCGAGGATTCTCGTGTGCCAGTGCTCAGAAGGCTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGAATACTCCT  
GTGTCACATGGACAGATCTTGCCCTGTCAGTGTCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG  
CAAAATTGGACTCTTGTGCTCTGGGGACCAACGGTTGTGAACATTGCTGTGAAGCAGTGAAGATTGTTGTGT  
GCCAGTGTCTTGAAGGTTATATACTCCGTGAAGATGGAAAACCTGCAGAAGGAAGATGTCTGCCAGTATAG  
ACCATGGCTGTGAACACATTGTGTGAACAGTGACGACTCATACACGTGCGAGTGCTGGAGGATTCCGGCTCG  
CTGAGGATGGGAAACGCTGCCAGGAAGGAAGGATGTCTGCAAATCAACCCACCATGGCTGCAACACATTGTGTTA  
ATAATGGGAAATTCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGGACGGAAGACGGTGCAAGAAAT  
GCACTGAAGGCCAATTGACCTGGCTTGTGATCGATGGATCCAAGAGTCTGGAGAAGAGAATTGAGGTCG  
TGAAGCAGTTGTCACTGGAATTATAGATTCTTGCAACATTTCCCCAAAGCCGCTCGAGTGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAAACCTCAACTCAGGAAAGACATGAAAAAAGCCGTGGCCC  
ACATGAAATACATGGGAAAGGGCTCTATGACTGGCTGCCCTGAAACACATGTTGAGGAGAAGTTTACCCAAAG  
GAGAAGGGGCCAGGCCCTTCCACAGGGTGCCCAGAGCAGCCATTGTTGTTCACCGACGGACGGCTCAGGATG  
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG  
AGGAGGAACATACAAGAGATTGCCCTGAGGCCACAAACAAGCATTCTTCTATGCCAGACTTCAGCACAATGG  
ATGAGATAAGTGGAAAACCTCAAGAAAGGCATCTGTGAAGCTCTAGAAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGGAACCTGCAAAACGGTCCAACAGCCAACAGAAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTGCACTGCAACACAGATATCTGTTGAAGAAGACAATCTTACGGTCTACACAAAAGCTTT  
CCCATTCAACAAAACCTTCAGGAAGCCCTTGGAAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT  
TCCAGAACCTGCAAACGAAGAAGTAAGAAAATTAAACACAGCGCTTAGAAGAAATGACACAGAGAAATGGAAGGCC  
TGGAAAATCGCTGAGATACAGATGAAGATTAGAATCGCAGACACATTGTTAGTCATTGTATCACGGATTACAAT  
GAACGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGTAAAACAATCAGTACTGA  
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATAACTAACTTGTATAAATTCTAGGAAAAAAATCCT  
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTTGTAATATAACTGTGGACAC  
AACTTGCTTCTGCCCTACCTGCCCTAGTGTGCAATCTCATTGACTATAACGATAAAGTTGCACAGTCTTACTT  
CTGAGAACACTGCCATAGGAATGCTGTTTTGTACTGGACTTACCTGATATATGTATATGGATGTATG  
CATAAAAATCATAGGACATATGTAATTGTGGAACAAGTGGATTAACTACAAATTAAATTCAACACTTCAG

## **FIGURE 15**

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPOALLESSCENKRADLVFII  
DSSRSVNTHDYAKVEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KMRHLSTGTMGLAIQYALNIAFSEAE GARPLREN VPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAI GVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN  
CAHFCINI PGSYVCRCKQGYILNSDQTT CRI QDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA  
LAEDGKRCVAVD YCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGC  
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI  
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRS DGKTCAKLDSCALGDHGCE  
HSCVSSEDSFVCQC FEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFR LA  
EDGKRCR KDVCKSTHHGCEHICVNNNGNSYICKCSEG FVLAEDGRRCKCTEGPIDL VFVID  
GSKSLGEENFEVVVKQFVTGIIDS LTISP KAARV GLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKGSM TGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEEELQEIA SEPTN KHLFYAEDFSTMDEI SEKLKKGICEALEDSDGRQDS  
PAGE LPKTVQQPTESEPVTINI QDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL  
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## **FIGURE 16**

GGAGCCGCCCTGGGTGTCAGCGGCTGGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCGTACTCCGTCCGGCCAGGGAGGGC  
**CATG**ATTCCCTCCCGGGCCCTGGTACCAACTTGCTGCCGTTTGTTCCTGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACCTGCCGCCAACCGGTTGCAG  
GCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCCATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC  
ATGCCCTCCCGAACCTGTCCCTGCCGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT  
TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGCTCCAGGGTGTGCCCAT  
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG  
GGTCTTAAGCCTCACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC  
AGTGGTTGGAGCTGTTGGGTACCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
TCTTGTACCACCGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCCCTGCCCTGGCCAAGAGAGCTCAGACACAATCTCAAGAATGGGACCC  
TTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGCCCTCCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGTCTCCAGGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**  
CCCACCACTATTGGCTAAAGGATTGGGTCTCTCCTCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCAACCTCTC  
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGTCTCCAGGC  
CCCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCGT  
ATTGATATAACCTGTCAGGCTGGTTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC  
TTATTAAAACATGAAATATGTGTTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC  
TGTTGTATGAAAAA

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSKP  
AVQYQ WDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGT  
AQCNVTLEVSTGPGAA VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDI  
KEDAIAPRTL PWPKSSDTISKNGTL SSVTSARALRPPHGPPRPGALTPTPSLSSQALPS  
PRLPTTDGAHPQPISPIPGGVSSSGLSR MGAVPVMVPAQS QAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## **FIGURE 18**

CGCCACCACTGCGGCCACC GCCAATGAAACGCCTCCGCTCCTAGGGTTTTCCACTTG  
TTGAATTGTTCTATACTCAAATTGACCAAGACACCTGTCTCCAAATGAAAATGTGA  
AATACGCAATGAAATTGAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA  
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCTGTGGCGAAATGCTAATTGC  
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA  
AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT  
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAAAACCTTAACAAAAATCAGATCCATAAAA  
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA  
TATAATTACATATATAGAAATTAGCTGAATCATCTCATTACTAGGTTACAAGAACAAACA  
CTATCTCAGCCAAGGGACACCCCTTCTAActCAACTCTTACTGAATTGTAACAAACCGTGAAT  
AATTTGTTCAAAGGGATACTTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC  
ACATCTTACAAAActCATGCACACTGTTGAACAAGCTACTTAAGGATATCCCAGAGCTTCC  
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT  
TCATATAACATGAAACATATTCTCATATGAATATGGATGGAGACTACATAAATATATT  
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTGCACTTTATATTATA  
AGAGTATTGGTCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGAT  
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC  
ACCCACATTATATGAACCTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA  
GGTATAGGAGTCTATGTGCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATT  
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCCATATGCATTTT  
ACCTTCTGGTTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAAACAAATTCTTGTG  
TAGCCTATTCTTGCTGAATTGTTCTTGTGGATCAATCAAATACTAATAAGCTCT  
TCTGTTCAATCATTGCCGACTGCTACACTACTTCTTAGCTGCTTGCATGGATGTGC  
ATTGAAGGCATACATCTCATCTGTTGGGTGTCATCTACAACAAGGGATTGGCA  
CAAGAATTTTATATCTTGCTATCTAACGCCAGCCGTGGTAGTTGGATTTCGGCAGCAC  
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAACAACCTTATT  
TGGAGTTTATAGGACAGCATGCCATTCTGTTAATCTCTTGCTTGGAGTCAT  
CATATAACAAAGTTTCTGTCACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGAGAAC  
TAAGGTCTGTGCAAGAGGAGCCCTCGCTCTGTTCTCGGCACCACGGATCTT  
GGGTTCTCATGTTGCACGCATCAGGTTACAGCTTACCTCTCACAGTCAGCAATGC  
TTTCCAGGGATGTTCAATTCTTGTTATCTGTGTTATCTAGAAAGATTCAAGAAGAAT  
ATTACAGATTGTCAAAATGCCCCGTGTTGGATGTTAAGGTAACATAGAGAAC  
GTGGATAATTACAACACTGCACAAAATAAAATCCAAGCTGTGGATGACCAATGTATAAAA  
TGACTCATCAAATTATCCAATTATTAACACTAGACAAAAGTATTAAATCAGTTTCT  
GTTATGCTATAGGAACGTAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT  
TTTCTATGTGAAATAGTTCTGTCAAATAGTATTGAGATATTGAGATATTGAAAGTAATTGGTT  
CTCAGGAGTGTATCTGCACCCAGGAAAGATTCTTCTAACACGAGAAGTATATGAA  
TGTCTGAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGTGCCTTGAAACTAGTCC  
CCTACCACTCGGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAACATGAAGGGCAGA  
ATATCAAACAGTGAAAAGGAATGATAAGATGTATTTGAATGAACTGTTCTGTAGAC  
TAGCTGAGAAATTGTTGACATAAAAGAATTGAAGAACACATTTCACCTTGTGAA  
TTGTTCTGAACCTAAATGTCCACTAAACAACTTAGACTCTGTTGCTAAATCTGTTCTT  
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA  
AAAAAAAAAAAAAAAAAAAAA

## **FIGURE 19**

MKRLPLLVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNECGNLTQSCGENANCTNTGSYYCMCVPGRSSSNQDRFITNDGTVCIENVANCHLDNVCIANINKTLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSSLGYKNNTISAKDTLSNSTLTFVKTVNPFQRDTFVVWDKLSVNHRRTHTKLMHTVEQATLRIQSFKTTEFDTNSTDIALKVFFFDSYNMKHIHPHMMMDGDYINIFPKRKAAYDSGNVAVAFLYYKSIGPLLSSSDNFLLPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAFWNYPDTMNGWSSEGCELTYSNETHTSCRCHLTHFAILMSGPSIGIKDYNILTRITQLGIIISLICLAIICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL LHYFFLAFAFWMCIEGIHLYLIVGVVIYNKGFLHKNFYIFGYLSPAVVVGFSaalgyryygtTKVCWLSTENNFIFIWSFIGPACLIILVNLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA LALLFLLGTTWIFGVVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNVPCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636, 648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181, 188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154, 155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329, 346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394, 434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTGATTTTATATTATAAGAGTAT  
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAAC TTGAAAAAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCTATGTGGCATTGGAAACTCACCTGATACC ATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTTGCCATATGCATTTTACCTTC  
TGGTTCTTCAGTGAATTCAAAGCACCAGGA

## FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGTGGGGAGGAGTTCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGTCACCCCGCTGGGA  
CAAGAAGCCGCCGCTGCCTGCCGGGGCCGGAGGGGGCTGGGCTGGGCGGGAGGCAG  
GGTGTGAGTGGGTGTGCGGGGGCGGAGGCTTGATGCAATCCGATAAGAAATGCTCGGG  
TGTCTGGCACCTACCGTGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG  
CCGCCGCCGCGTCAGAGCAGGAGCGCTCGTCCAGGATCTAGGGCACGACCATCCAACCC  
GGCACTCACAGCCCCGAGCGCATCCGGTCGCCAGCCTCCGCACCCCCATGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGCGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGCGCCCCCTGCCCTCTCGGACGCCGGGCC  
CCACGTGCACTACGGCTGGGCACCCCATCCGCCTGCCACCTGTACACCTCCGGCCCC  
ACGGGCTCTCCAGCTGCTTCTGCCATCCGTGCCAGGGCTCGTGGACTGCCGCCGGGC  
CAGAGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCACCGTGGCATCAAGGG  
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCAGGGCAAGATGCAGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTCAGGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAACGCCCTCCGGCTCCCTGAGCAGTGCCAAACAGCGGAGCTGTACAAGAA  
CAGAGGCTTCTTCACTCTCATTCCGCCTGCTGCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGCCACTTGAATCTGACATGTTCTTCCGCCTGGAGACCGACAGCATG  
GACCCATTGGCTTGTACCCGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTAA  
GAGACCATGCCGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGACG  
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA  
GTTGTACATATTCAAGAGTTTCCATTGGCAGTGCCTAGTTCTAGCCAATAGACTGTCTGAT  
CATAAACATTGTAAGCCTGTAGCTTGCCTGCCAGCTGCTGCCCTGGGCCCTATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGCTCAGTTCTGCTGAATAACCTCCATCGATGGGAAC  
TCACTTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAAATTCTCATCACTTC  
CCCAGGAGCAGCCAGAACAGCAGGAGTAGTTAATTCAAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAATTCACTCAACCCATGTGGAATTGATCTATATCTACTTCCAGGG  
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGGCCACCAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGGCCACTCCAGGCCCTGGGACAACCTGAGAATTCCCC  
CTGAGGCCAGTTCTGCATGGATGCTGCTGAGAATAACTGCTGTCCGGTGTACCTGC  
TTCCCATCTCCAGGCCACCAGCCCTGCCCACCTCACATGCCCTCCCATGGATTGGGCCT  
CCCAGGCCCTTACCTTATGTCAACCTGCACTCTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTGAGCAGCGGGGAAGACCTAGAAC  
CCTTCCCCCAGCACTGGTTTCAACATGATATTATGAGTAATTATTTGATATGTACA  
TCTCTTATTCTTACATTATTATGCCCAAATTATATTATGTATGTAAAGTGAGGTTG  
TTTGTATATTAAAATGGAGTTGTTGT

## **FIGURE 22**

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## **FIGURE 23**

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGACCCCTGACCTCCTCA  
GAGCAGCCGGCTGCCGCCCGGAAGATGGGAGGAGGAGCCACCGCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTCTGCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA  
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCCTTGTCTAC  
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG  
GATCAAAATGTGACAAGAAGTGATGCGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATAACAGTCACCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGAATCCAGCTCCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAACT  
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGGCCGAATTG  
TGGATATCGCAGGTGCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA  
TCATAGCAGCGTAGTAGTTGTGGCCTTAGTGATTCCGTTGTGGCCTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTAAAATGTGCAGTGGCTACGCCGTAAATCCCAGCACTTGGAAAGG  
CCGGCGGGCGGATCACGAGGTAGGAGTTCTAGACCAGTCTGCCAATATGGTAAACCC  
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTCCAGCTGC  
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAAATAAAATAATA  
AATAAAATCTGGTTTACCTGTAGAATTCTTACAATAAATAGCTTGATATTG

## FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDJQQVVTAVEYQEAILACKTPKKT  
VSSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQ  
GQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD  
GIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN  
SVGYRRCPGKRMQVDDLNISGIIAAVVVA  
LVI  
SVCGLGVCYAQRKG  
YFSKETSFQKSNSSSKATTMSENVQWLTPV  
IPALWKA  
AAAGGSRGQEF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## **FIGURE 25**

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAAAGAG  
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCCACAGCCGGACCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAACATGGGATTAAATATTTACTTCTAAATAA  
ATGAATTACTCAATCTCCTATGACCACATCTACATACACTCCACCTTCAAAAAGTACATCAATA  
TTATATCATTAAGGAAATAGTAACCTCTCTTCTCAATATGCATGACATTGGACAATG  
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTATCA  
TTGACAAATGCAAGCATCTCCTTATCAATCAGCTCTATTGAACTTACTAGCACTGACTG  
TGGAACTCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCTATGTGCTACTTGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCCAGATTGCC  
AGCTAACACACAGATTCTCTCACAGACTAACATATTGCAAAAATTGAATACTCCACAG  
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTTCAGTCACCAAT  
ATTAATGTAAGGAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTACTGA  
ACTGCCTGAAAATGTCGCAACTGAGCAACTACAAGAACTCTATATTAAATCACAAC  
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCTACATAATCTCTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT  
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTCTTATCA  
ATCTCGCAGCCTGGTTAGCTGGTATAACCTCACAGAAATACCAGATAACGCCCTGGTT  
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCCATGT  
TGCTCTTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAACTCTATTAAATAGAA  
TACGAAGGGGTGATTTAGCAATATGCTACACTAAAAGAGTTGGGATAAAATAATATGCCT  
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAC  
TACTAACAAACCTAGATTGTCTTACATTCAACCCATGCATTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCTGAGTCTCG  
CCAAACCTCAAGGAAATCAGCATAACAGTAACCCATCAGGTGTGACTGTGTACCCGTTG  
GATGAACATGAACAAAACCAACATTGATTGAGCCAGATTCACTGTTTGCCTGGACC  
CACCTGAATTCCAAGGTCAAATGTTGGCAAGTGCATTTCAGGGACATGATGGAAATTGT  
CTCCCTTCTTATAGCTCCTGAGAGCTTCTTCTAATCTAAATGTTAGAAGCTGGGAGCTATGT  
TTCCTTCACTGTAGAGCTACTGCAGAACACCAGCCTGAAATCTACTGGATAACACCTTCTG  
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCCTTCTGAGGGAAACACTA  
GATATAATGGCGTAACCTCCAAAGAAGGGGTTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAAATG  
GCTCTTGAATATTAAAATAAGAGATATTGAGCAGGCCATTCAAGTTGGTGTCTGGAAAGCA  
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA  
TGCTCGCAAAGTGCCTGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAAACAGAAAAAAA  
TGTGTAAATGTCACCACCAAGGTTGCACCCCTGATCAAAAGAGTATGAAAAGAATAATAC  
CACAAACACTTATGGCCTGTCTGGAGGCCTTCTGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTCCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG  
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGATAAAATCTCTGGGAAGCAGGAAA  
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCT  
AAAAACCAAGGAAACCTACTCCAAAATGAAC

## FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQTNNIAKIEYSTDTPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRSVIAGINLTEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVNLKFLLDNKNPINRIRRGSFSNMLHLKELGINNMPELISIDSALVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSAHYHTIESLPNLKEISIHSPNIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVROVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV  
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLIN  
LWEAGKEKSTSLKVATVIGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC  
CACGCTTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTACAAAGTTTGTCTTA  
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG  
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT  
GCCTCAAAGGAGTAGCTGAAACCTTGAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCAAAAAATGCCTCAATAACCTGAAGGCCAGGGCAGAATTGCCAACACCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGTAACCGTCCGTGGATGAAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTGGCTGGTTCACTATGGTATCTCATATGTGGTATTATGTGAGGCAAAATCAGGAG  
GATGCCGGAGACACCTCGAATACTTGAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA  
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGAAACATTTGAA  
ACTTTGTATTCAGTTTTGAATTATGCCACTGCTGAACCTTAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTATTTTT  
AATTAAAAGCAAATAAAAGCTTAACCTTGAACCATGGAAAAAAAAAAAAAAACA

## FIGURE 28

MNLVDLWLTRSLSMCLLQS FVLMILCFHSASMC PKG CLC SSS GGLN VTCS N ANLKEIPRDL  
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF  
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## **FIGURE 29**

ACCGAGCCGAGCGGACCGAAGGCAGCAGGGATTGAGGTGAGCAAGAGGATGCTGGCGGGG  
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCACCTCCTGCTGGTGCT  
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCGCCCCGCTGCGAGTGCTCCGCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG  
ACCGCCTGCTGGACCTAGGAAGAACGCATCAAACGCTAACCGAGCACGAGTTCGCCAG  
CTTCCGACCTGGAGGAGCTGGAGCTAACGAGAACATCGTGAGCGCCGTGGAGGCCGGCG  
CCTTCAACAACCTTCAACCTCCGGACGCTGGGTCTCCGAGCAACGCCCTGAAGCTCATC  
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCAGAACAAAGAT  
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCACCGCGCCTCAGCGGCCTAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCGTGTCCCACCTGCACGGCCT  
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC  
TGTACCGACTCAAGGTCTTGGAGATCTCCACTGGCCTACTTGGACACCAGACACCCAAC  
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCCCTAACCTCTCCATACACCCCCATCA  
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGCG  
GGGCAGCTGGCGTGGTGGAGCCCTATGCCTTCCCGGCCCTAACACTACCTGCGCGTGTCAA  
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG  
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCTGTGGTGGTCCGG  
CGCCGCTGGGGCTCAACTTCAACCGGCAGCAGCCCACGTGCGCCACGCCAGGTTGTCCA  
GGGCAAGGAGTTCAAGGACTCCCTGATGTGCTACTGCCAACTACTCACCTGCCGCCGCG  
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGGACGAGGGCACACGGTGCAGTT  
GTGTGCCGGGCGATGGCAGCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTTCCGTGATGGCACGCTGGAGGTGCGCT  
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGCCAACGCCGGGCGAACGAC  
TCCATGCCGCCACCTGCATGTGCAGCTACTGCCGACTGCCCATCAGCCAACAA  
GACCTTCGCTTCATCTCAACCAGCCGGCGAGGGAGAGGCCAACAGCACCCGCCACTG  
TGCCTTCCCTCGACATCAAGACCCTCATCGCCACCACATGGCTTCTCATCTTT  
CTGGCGTCGCTCTCTGGCTGGTGTGCTGTTCTGGAGGCCGGCAAGGGCAACAC  
AAAGCACAAATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG  
ACGGCCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGGGGGGCAGGGACCCCCG  
GGCGGCCGGCAGGGGAAGGGCTGGTCGCCACCTGCTCACTCTCCAGTCCTTCCACCTC  
CTCCCTACCTCTACACACGTTCTCTTCTCCCTCCGCCCTCGTCCCTGCTGCCCG  
CCAGCCCTCACCACCTGCCCTCTTCTACCAGGACCTCAGAACGCCAGACCTGGGACCCCA  
CCTACACAGGGCATGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTCA  
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACTTGGTTCAATAATTATGGATT  
TATGAAAATTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPI~~LLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF~~  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL  
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGNLETLLDSNPLA  
CDCRLLWVFRRRWRLNFNRRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL  
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFC~~L~~VLLFLWSRGKGNTKH~~NIEIEYV~~PRKSDAGISSADAPRKFNMKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

### FIGURE 31

CCCGACGCGTCGGCACCTCGGCCGGCTCCGAAGCGGCTCGGGGCGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTCGCCAGGCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC  
TGTCGCCTGCTGGCGCCGGCGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGCTCAAGTGCCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTACTTTGGGGAGAAGA  
GAGCCCTCGAGATAATCGAATTCACTGGTTACCTCTACGCCAACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT  
ATAAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG  
CCTGCAGCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCGCAT  
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTGGTACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCAGTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCA  
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGC  
CCTCCTCCAGCACCTACCACGCCATCATCGTGGAATCGTGGCTTCATTGTCTCCTGCTG  
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCCAGGGCCATCATCAATGCAGAAGGCC  
GGCAGTCAGGAGGGACGACAAGAAGGAATATTCATCTAGAGGCCCTGCCACTTCCTGC  
GCCCCCAAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCGTACAGAAATGTCTGC  
TTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGGCCCTGGGTGAGAAAAGCAAAAAACA  
AACAAAAAAACA

## FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRQLVTSTPHELSIISNVALADEGEYTCSIFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTCCTTCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGAAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGTTAAAAATGCTGCTTGGATTCTGTT  
GCTGGAGACGTCTTTGCTTGCCGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCAATTATTCATGGCAATT  
CCTCACTCGACTTTCCATAATGAGTTGCTAACCTTATAATGCGGTTAGTTGCACATGG  
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTCTGGGGCTGCAGCTGGTAAAAGG  
CTGCACATCAACAACAAGATCAAGTCTTTCGAAAGCAGACTTCTGGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG  
ACTTGAACAAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCACTGCCAAC  
GTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC  
CTGATCGGCCAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGTCCTTGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG  
CCCAAGAACAGGACCTTGCTCCTGGACCCCTGCCACTCCTTCAAGACAAATGGCAAGAG  
GATCATGCCACACCAGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT  
CAAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC  
GTTTACCCCTGCCCTGGGGCTGCAGCTGCGACCACATCCCAGGTCGGTTAAAGATGAAAC  
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCCAGCTCTAACGTGCAGGA  
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTGTGGATTACAAGA  
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACACACTTCAAG  
AACCTTTGGACCTCAGGTGGCTACATGGATAGCAATTACCTGGACACGCTGTCCGGGA  
GAAATTGCCGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACAACCTG  
CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA  
CAATTACTCATGTACCTCCGGTGGCAGGGGTCGGACCAAGTTAACCTCCATCATCCAGA  
TAGACCTCCACGGAAACCCCTGGAGTGCTCCTGCACAATTGTGCCTTCAAGCAGTGGGCA  
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT  
TAGAAAGGATTTCATGCTCCTCTCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCCACGTTAACCTGCACAGTAAAACAGCACTGGGTTGGCGAGACCGGACGCACCTCC  
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGCCACTGCTGCTGGT  
GTTGTCACCTCCGCCTTCACCGTGGTGGGATGCTCGTGTGTTATCCTGAGGAACCGAAAGC  
GGTCCAAGAGACGAGATGCCAACTCCTCCCGTCCGAGATTAACTCCCTACAGACAGTCTGT  
GAECTTCTACTGGCACAATGGGCTTACAACGAGATGGGCCCCACAGAGTGTATGACTG  
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAAAGGCG  
ATACATCCTTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCCGCG  
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAAACGAAAGGGCT  
GACCCCTTACTTAGCTCCCTCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA  
GCCAGCTCGCTTTGCTGAGAGCCCCCTTGACAGAAAGCCCAGCACGACCCCTGCTGGAAG  
AACTGACAGTGCCCTCGCCCTCGGCCCCGGGGCTGTGGGTTGGATGCCCGGTTCTATAC  
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTCCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAAATAAGTAACTTGACTTCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVGVDVCKEKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFGLQLVKRLHINNNKIKSFRKQ  
TFLGLDDLEYLQADFNLLRIDPGAFQDLNKEVLILNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSLPPAPAQEETFAPGPLPTPKTNQEDHATPGSAPNGGTK  
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHIPGSGLKMNCNNRNVSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLEYLNVEYNQIQILPGLTFNAMPKLRILILNNNLLRSLPVDFAGVSL  
SKLSLHNYYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPLTSHSKNSTGLAETGTHNSYLDTSRVSISVL  
VPGLLLVFTSAFTVVGMLVFILRNRKRSKRDANSASEINSLQTVCDSYWHNGPYNADG  
AHRVYDCGSHSLSD

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## **FIGURE 35**

AGTCGACTGCGTCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTGCGGGCTAAGGGAAACTGTTGGC  
CGCTGGGCCCGCGGGGGATTCTTGGCAGTTGGGGGTCCGTGGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACC CGCTCCAGACAC  
AGCTCTGCGTCCCTCGAGCGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGC GGCCCTCAG  
**AGAATGAGGGCGGCCGTTCGCCCTGTGCCTCCTGGCAGGCGCTCTGGCCCGGGCGG**  
CGGCGAACACCCCCTGCGACCGTGCTGGCTCGGCTCGGGCCTGCTACAGCCTGC  
ACCA CGCTACCATGAAGCGGCAGGGCGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCGTGC GTGC GGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCAGG  
GCCGGAGGGGCTCAAAGACCTGCTGTTCTGGT CGCACTGGAGCGCAGGCGTTCCC ACT  
GCACCC TGAGAAGCAGCCTTGC GGGGTTCTCGCTGTCTCCGACCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCAACGCTCCTGCACCGCGCGGAGATGCGC  
GGTACTCCAGGCCACCGTGAGGCGCAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGTCCTGCGCCGCCCCGG  
GCCGCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGC GCTCTGCCGGGACAGCTCCGATCTCAGTTACTGCA  
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTCCCTGCC  
GGGAGGTACCTCCGTGCTGGCAAATCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG  
CTTGCCTCGGAATGTGCTACGGGCTTCGAGCTGGGAAGGACGGCCGCTTGTGACCA  
GTGGGAAGGACAGCGACCCCTGGGGGACCGGGTGCCCACCAGGCGCCGGCCACT  
GCAACCAGCCCCGTGCCG CAGAGAACATGGCAATCAGGGTGACGAGAACAGCTGGGAGAGAC  
ACCACTTGCCCTGAAACAAGACAATTCA GTAACATCTATTCTGAGATTCTCGATGGGAT  
CACAGAGCACGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAGGCCACTATCACC  
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTT  
CGACTCCTCTGCGGTCTTCAATTGTGAGCACAGCAGTAGTAGTGTGTTGGTATCT  
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCA GAAAGCCCTTCCAGCCA  
AGGAAGGAGTCTATGGGCCCGCCGGCCTGGAGAGTGATCCTGAGCCCCTGCTTGGCTC  
CAGTTCTGCACATTGCAAAACATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCTTGTGGAGTCCCTTGGCTCTAGTGATGCAATGGAAACAGGGGA  
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC  
TTGTGTA CTGACAATTCTGAGAAATCCCCCTTCTAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAAC TGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA  
TGGTGATACTGGGGACCGGGTAGTGCTGGGAGAGATATTTCTTATGTTATTGGAGAA  
TTTGGAGAAGTGATTGAACTTTCAAGACATTGGAAACAAATAGAACACAAATATAATTACA  
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT  
ATTGGTTGAAATCCCAGGGAAAAAATAAAAATAAAGGATTGTTGAT

## FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPGA  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVFIFVSTAVVVLVILTMVLGLVKLCFHESPSSQPR  
KESMGPPGLESDEPEPAALGSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## **FIGURE 37**

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGEVNDARRIGKYCGDSPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRTGTLEGN  
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

**Signal sequence:**

amino acids 1-23

**N-glycosylation site.**

amino acids 355-359

**Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

**Tyrosine kinase phosphorylation site.**

amino acids 199-208

**N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

**Cell attachment sequence.**

amino acids 149-152

## **FIGURE 39**

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCGCGGCTGGGGCGGTGCGCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACCTG  
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACCTTGAG  
GTGGAAACACTGCCTGGAGGAAGAGAATTGTCAAATAAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCTGC  
CTTCCCTGTCTGGGGAACAGAGAGGCCCTCGGGTGGCTACGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGCACTGTGACTGCCAAGCCGGCTACGGGGTGAGGCCGTGGCC  
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGCCACAGAGGGAGCCAAC  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGCTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCAGTGGTGGTCAACGCCATCTCATTGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGGAGGGCTTCATCAAGGGCAGAT  
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCGAGAGCTGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTTCCACCTGGCGGGACTGGCAGGCTCACAATGTGTGA  
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCCAGTTCTGT  
TCTGTGTTCACCATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA  
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQS PPPQPHPCHTCRLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCCGGTERPCGGYGCCEGEGTRGGSGHCDCQAG  
YGGEACGQCGLGYFEAERNASHLVCACFGPCARCSGPPEESNLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG  
IIICALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-363

**N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGCACTCTGGTGTGCCCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGCAGCTCAAAGAGGT  
GCCCACCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTGGAGGCCAGCACACACCTGCTGGTGTTCGG  
CATGGAGCAGCGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCGTCTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGCTGTCCCCGCCAGCGCCCGGGCC  
CGGGTGACCGTCGAGTGGCTCGCGTCCCGCACGACGGCTCCAACCGCACCTCCCTATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGTGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC  
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGGACTATGGAG  
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGATGAAGTGGGCCAGAACTGGGTGCTGGAGCCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTAAGTGGC  
CGTTTCTGGGGCCTCGACAGTGCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGCCAGGCCATAGGCCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGAGGGTACCAAGGAGAGCTG  
GCGATGACTGAAGTGCCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAATTGGCTTCTCAGGAATGAGAATCTTGCCACTGGA  
GAGCCCTGCTCAGTTCTATTACTGCAGTATATTCTAAGCAGTACCT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTATTGTTACTTGCTGTAC  
TGGATCTGGCTAAAGTCCACCACCACTCTGGACCTAACAGACCTGGGGTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAGACTTTGAAAACATGAATAAAACACATTATTCT  
AAAAA

100 700 2000 5000 10000

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLRLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFQSFSREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

**N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

**Amidation site.**

amino acids 74-78

**TGF-beta family signature.**

amino acids 282-298

## **FIGURE 43**

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTCAGTGGCCTGATCGCGATGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCGATCCTGTTGCTCCCTGG  
CATTGGGCAGTGTACAGTCACTCTTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT  
GTGAAGTTGTCCTGTCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAAAGTTGACCA  
AGGAGACACCACCACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG  
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTTCTGAATAACACCTGGTCAAAGAT  
GGGATAGTGATGCCAACAGAACAGATGGTCCCCACCTTCTGAACTCTCCTATGTCT  
GAATCCCACACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATAACTGGAGAACACA  
GCTGTGAGGCACGGAATGGTATGGGACACCCATGACTTCAAATGCTGTGCGATGGAGCT  
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCCTGATTCTCCTGGGAAT  
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAACCAAACAG  
ACCTCGTCATTCCCTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCCTACT  
CAGGTGCTACGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCCTATTGTCTTC  
TACACCCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGCC  
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTTGTAA  
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGAAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTTCTGGCTCTTCCCTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG  
TGATGACACTGGGTCCTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG  
CCACTGGATCCCTGCCCCTGCTGAATACAAGCTGACTGACATTGACTGTCTGT  
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACCTGAAGCCAAAAG  
GATTAAAACCGCTGCTCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTACGCCTG  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGATCAGCCTGACCA  
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW  
KFDQGDTTRLCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTSEQDGSPPSEYTWFKDGIIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## FIGURE 45

CAGCGCGTGGCCGGCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGCTCTGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG  
GCTCGTGCCACCCACCAAGTTCCAGTGCCGCACCAGTGGTTATGCGTGCCCCCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCGGAAG  
GGGATGCCACAACCAGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC  
ACAACCAGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCTATGGGTTATTGCAGCTGCTGCGGTGC  
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTGTCCCTGGCTCCGAGCCAGGAGCGC  
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC  
CTCGCTGCCTGAGGACAAGCAACTGCCACCCAGTCACTCAGCCCTGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACAGAC  
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGCCCTGTGCTTAAGAACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAGTTGCTTC

700 720 740 760 780 800 820 840 860 880

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLLLLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLDLSDGSDEEECRIEPCQKGQCPPPGLPCPCTGVSDCSGGTDKKL  
RNCSRILACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPVTLESPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

**Signal sequence:**

amino acids 1-30

**Transmembrane domain:**

amino acids 230-246

**N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

**Leucine zipper pattern.**

amino acids 17-39

## **FIGURE 47**

CCACCGCTCCGGTCTCGCTCGCTCGCAGCGGCGGCAGCAGAGGTGCGCACAGATGCGG  
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTAGCTGGCGCTGTGCTTCGCCCTGCACAGCTCACGGCGGGTT  
CGATGACCTCAAGTGTGTGCTGACCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA  
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA  
ACAAGACATATAGACATGGAGAGAACGTAATCATCACTTGTATGAAGGATTCAAGATCCGG  
TACCCCGACCTACACAATATGGTTTATTATGTCGCGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC  
TCCAGACCTCCTTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACCTT  
GATGGGTCTCGTATCTTGAGTGCTTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTG  
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCAAATGGTGAGTCACGGAGATTCGTCT  
GCCACCCGGCCTTGTGAGCGTACAACCACGGAACTGTGGTGGAGTTTACTGCGATCCT  
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGGCTCCCCGGAG  
TTCCAGCAGTGACCTGACTTGTGGTAGACGGCGTGCCTCATGCTCCGTCTATG  
ACGAAGCTGTGAGTGGCGCTTGAGTGCCTAGGCCCGGGTACATGGCCTCTGTGGGCCAG  
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA  
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGAGCTGCTCCAAA  
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCTGCTGGACAACCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCACTGGGT  
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTCTGAAGTGTCTTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTTGTGGTTAGACAAATGTAAACAA  
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTGGAGGGCTGGAAGCTTGATCAAGTC  
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHQCQDGFKLGATKRLCLKHFNGLGWI PSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS  
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAAEVASTSPGIHHAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## **FIGURE 49**

CCCCACGCGTCCGCTCCGGCCCTCCCCCCCCTCCCGTCGGTCCGTGGTGGCCTAGAGA  
TGCTGCTGCCCGGGTTGCAGTTGTCGCGCACGCCCTGCCCGCCAGCCCGCTCCACCGCCGT  
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAAACCGCGCTACAGG  
CCGTGCTGCCGTGCTGGCTGGTGGGCTGCCGGCCGACGGGTGCCCTGCTGAGTGCC  
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTAA  
TAAAGTCATTTACTTCATGATACTTCTCGAACAGACTGAACATTGAGGAAGCAAAGAACCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA  
AAGTTCATTGAAAACCTCTGCCATCTGATGGTGAECTCTGGATTGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT  
ACAATTTAGGAACTGGTATGTGGATGAGCCGCTGCCGGCAGCGAGGTCTGCGTGGTCATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA  
CCGGTGCAACATGAAGAACAACTTCATTGCAAATATTCTGATGAGAAACCAGCAGTCCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG  
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCCTGAATCTGCCCTACAT  
CCTAATCCCCAGCATTCCCTCTCCCTCCTGTGGTCAACCACAGTTGTATGTTGGTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC  
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTCATTCCGAGTGTGTT  
CGGGAGAAGCCACTCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGTTGTGACTCTGGTGAGCGTGGAGAGTGAGATTGTGACCAATGACATTATGA  
GTTCTCCCCAGACAAATGGGAGGAGTAAGGAGTCTGGATGGTGAAATGAAATATATG  
GTTATTAGGACATATAAAAACTGAAACTGACAACAAATGGAAAAGAAATGATAAGCAAAATC  
CTCTTATTTCTATAAGAAAATACACAGAACGGTCTATGAACAAAGCTTAGATCAGGTCTGT  
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTGGCTGTATCCTTTAT  
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTTGCCCAGGTCTGGCACATAGTA  
GAGTCTCAATAATGTCACTTGGTTGGTGTATCTAACCTTAAGGGACAGAGCTTACCTG  
GCAGTGATAAAAGATGGGCTGTGGAGCTGGAAAACCACCTCTGTTTCCCTGCTCTACAG  
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGQTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY  
SDEKPAVPSREAEGEETELTPVLPETQEEDAKTFKESREAALNAYILIPSIPLLLLLLV  
VTTVVCWVWICRKRKREQPDYSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSCGEATPDDMSCDYDNMAVNPESGFVTLSVESGFVTNDIYEFS PDQMGRSKES  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## **FIGURE 51**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCGCTGAGCCCCGGCGCCCGAGAAGACTTGT  
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTGCGTTGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC  
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATAATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCATT  
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAAAGACATTCCCTTC  
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG  
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTAGAAGTCTTGATCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTGATAAAAGTGGACTTCTCATCCTCCT  
GGACAACGTGGCTGCCAGCAGGACACAAACCTCCAAAGCTGCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGACTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCATTCCCTCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG  
TGACCTTCATACCGCTTTAATGACCTGGGATTTGACCACAAATGCCACCGTTGCT  
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAGTGCCTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSAYCLHQRRAVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSFYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRQTAISLQPGISEDLKKVKDRMGIDSSDKVD  
FFILLDNVAEQAHLNPSCPMLKRFARMIEQRRAVDTSLYILPKEDRESLQMAVGPFLHILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTIFIPLLMTLGIFDHKWPPFAVDLTMEYLQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## FIGURE 53

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTCTAGCCT  
TAAATTCAGCTCATCACCTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTTGCACCAGACCTGGATTCCTAGCGTCTCCATCTGGAGTGC~~GG~~CTGGTGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACC~~GT~~TGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGT~~CCT~~CATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATA~~C~~ATTGGCTCAGTGTGAGCAAGAAGAAGTTATG  
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA  
GTCCCAGAGGGTGT~~C~~AGGCTGGCTGACGCCCTGGCATTGCAAGGGAC~~G~~CGTGGAA~~G~~TGAA  
GCACCAGAACCA~~G~~GTGGTACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGAAAGGTGG  
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACC~~TT~~CA  
GGATTGCCCTCTGGCCTTGGGGAAAGAACACACTGCAACC~~A~~ATGATGAAGACACGTGGTCG  
AATGTGAAGATCC~~TT~~GACTTGAGACTAGTAGGAGGAGAACCTCTGCTCTGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACA~~A~~CTGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGAGTCCCTCTCCCTCAGAGACCGGA  
AATGCTATGCCCTGGGTTGGCCGCATCTGGCTGGATAATGTC~~T~~GCTCAGGGAGGGAG  
CAGTCCCTGGAGCAGTGC~~C~~AGCACAGATTTGGGGTTTCAGACTGCACCCACCAGGAAGA  
TGTGGCTGT~~C~~ATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT  
TCTTCTGCCCTGGACTGGACTTAACTTGGTGC~~CC~~CTGATTCTCAGGCC~~T~~CAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGA~~A~~CTACATCA  
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT  
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCA~~TTT~~GT~~C~~CTGTTCTGAAGAA~~CT~~GTGACAAAATACAGATTTGGTACTGAAAGAGA  
TTCTAGAGGAAC~~GG~~AATTTAAGGATAAAATTCTGAATTGGTTATGGGTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAAC~~TT~~ATTTACAATAAAAGATAGCAC  
TATGTGTTCAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPSGVRLVGGHRCEGRVEQKGQWGTVCDDGWDIKDVAVL  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## **FIGURE 55**

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGAC  
CCACCGTCCCGGGACCGTGGCGGACCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGG  
CGTCTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGCCCTAGAACAGACTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGCCATAGTGAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGG  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCCTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTG  
CTGTCGCGGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTGTAAATGCCATCACCAGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCAAGGCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTCCTGGCTGTTATCTCGAA  
CTCTGGCTCCTGGCTCTTCAGCCTCATGGCCTCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAACGACTCTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGCTCTACAAGTGG  
AAAGACTGAAGAAACACATCTGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATATGGAGCTGGGTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAGGGCGGCCGCACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGGTTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI  
VAAAEEILQCFGYVDIL  
VNNA  
GISYRG  
TIDTTVDVKRM  
ETNYFGPVALTKALLPSMIKR  
RQGHIVAISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLA  
AVGKKKD  
VILADLLPSL  
AVYLRT  
LAPGLFFSL  
MASRARKERKS  
KNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## **FIGURE 57**

CCCCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA  
AAAAAAAAAACACACCAAACGCTCGCAGGCCACAAAAGGG**GATGAA**ATTCTTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCCCTAA  
GAGGAGAAAATCAGTCACCGGCAGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTGCTAAACTTAAAGCAAGCTGGTCTCTGGATATAAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGTGCCAAGGTCATACCTTGTTG  
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA  
GGCATTCTCCTGCAATGACGAAGAATAACCATGCCATTGTCACTGTGGCTCGGCAG  
CTGGACATGTCTGGTCCCCTTACTGGCTTACTGTTCAAGCAAGTTGCTGCTGTTGGA  
TTTCATAAAACTTGACAGATGAACGGCTGCCTTACAAATAACTGGAGTC  
AAAACACATG  
TCTGTGTCCTAATTGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG  
ATTTTATTCCATCTCTATAGCTTTTAACAACATTGGAAAGGATCCTCCTGAGCGTT  
CCTGGCAGTTAAAAGAAAAACTAGTTAAGTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCA**AA**GCACCTAGTTCTGAAAACGATTACAGGTTAGGTTAGGTGATGTCATCTA  
ATAGTGCAGAATTAAATGTTGAACCTCTGTTTTCTAATTATCCCCATTCTCAATA  
TCATTGAGGCTTGGCAGTCTCATTACTACCACTGTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAACCTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA  
CCAAAATGACTTTATTAAAATAATTCCAAGATTATTGTTGAGCTCACCTGAAGGCTTGCAA  
AATTGTAACATAACCGTTATTAAACATATATTGTTGAGCTCACCTAAATTGTTG  
ATAATTGTTGTTCTTTCTGTTCTACATAAAACGTTAGAAACTCAAGCTCTCTAAATAAAA  
TGAAGGACTATCTAGGGTATTTCACAATGAATATCATGAACCTCAATGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACCTCACATTCCAATGCCAACATTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCACTGGGATTAAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA  
AA  
AA

## **FIGURE 58**

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

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## **FIGURE 59**

CCACCGCTCCGGACCGTGGTCGACTAGTTAGATCGCGAGCGGCCGCCGCGCTC  
AGGGAGGAGCACCGACTGCGCCGCACCCCTGAGAGATGGTTGGTGCCTGTGGAAAGGTGATTG  
TTTCGCTGGTCCTGTTGATGCCCTGGCCCTGTGATGGGCTGTTCGCTCCCTACAGAAGT  
GTTCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAACATTGAGTTGGTCGGCCCTTCCCAGGACTGAACATGA  
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTGGTTC  
TTCCCAGCTCAGATACAGCCAGAACGATGCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG  
AGGTTCATCCATGTTGGACTCTTGGAACATGGCCCTATGTTGTCACAAGTAACATGA  
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT  
AGCACGGGATTATAACAGTGCACTAATTCAAGTTTCAGATATTCTGAATATAAAAATA  
ATGACTTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC  
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA  
TGGATATTCTGATCCGAATCAATTATAAGGGGCTATGCAGAAATTCTGTACCAAATTGGCT  
TGTTGGATGAGAACGAAAAAAAGTACTTCCAGAACAGCAGTGCCTGAATGCATAGAACACATC  
AGGAAGCAGAACTGGTTGAGGCCTTGAATACTGGATAAAACTACTAGATGGCAGTTAAC  
AAGTGATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCCTG  
GCACCGAACCTGAGGATCAGCTTACTATGTGAAATTGGTCACTCCCAGAGGTGAGACAA  
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACTATAGTTGAAAAGTACTTGCAGA  
AGATACAGTACAGTCAGTTAACGCATGGTTAAGTGAATAATTATAAGGTTCTGA  
TCTACAATGCCAACGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTGATGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAACGGCAGAAAAAAAGTTGGAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGAATTCCATCAGGTAATTATTC  
GAGGTGGAGGACATATTTACCCATGACCAGCCTCTGAGAGCTTTGACATGATTAATCGA  
TTCATTATGGAAAAGGATGGATCCTTATGTTGATAAAACTACCTCCAAAAGAGAACAT  
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCAAGGAATAAAAAAA  
TTATCTTTCATATCTGCAAGATTTCATCAATAAAAATTATCCTGAAACAAGTGAGC  
TTTGTTTTGGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAATGA  
AATTTAGGGTCTTGAATAGGAAGTTAATTCTTAAGAGTAAGTGAAGGAGTGCAGTTG  
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAACAGTTGGCATGCCGTGAAGGT  
GTTTGGAAATATTATGGATAAGAACAGCTCAATTATCCAAATAATGGATGAAGCTATAA  
TAGTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAACATTCTTGAAATA  
AAAATATTATATAAAAGTAAAAAAAAAA

## **FIGURE 60**

MVGAMWKIVSLVLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGREL  
VGPPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTTSNMTLRDRDFPWTTLSMLYIDNPVGTGSFTDDTHGYAVNEDDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNPNVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLDGDLTSDPSYFQNVTG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIYNGQLDIIVAALTERSLMGMDWKGSQEYKKAEKVKWKIFKSDSEVAGYIRO  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## **FIGURE 61**

CGAGGGCTTCGGCTCCGAATGGCACATGTGGAATCCCAGTCTGGTGGCTACAACAT  
TTTCCCTTCTAACAAAGTCTAACAGCTGTTCAACAGCTAGTGATCAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGANAGCTCCTTG  
CCTCTCTGTTGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGGAGGGCCTGCCTAACAAAGCTTCAAAAAACAGGAGCAGTCCACTGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGAAAGACTGGGTTAGTCCTAATATCAAATTGACTGGCTGGG  
TGAACCTCAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTGTAAAATAAATTTAAAAAAGCAAGTATTTCATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGGAGAAAGTATGTTAAAATA  
GAAAAACAAAATGCAGAAGGAGGAGACTCACAGAGCTAACACCAGGATGGGACCTGGGTC  
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT  
GCAGAATCATGTGAGGGCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCAGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG  
ACAGCCGCTCTGTTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC  
ATGCCCTCAGTTCAAGCACCTTCACTCTGAGAACTGTGACTGGACCTCAACCACCTGACCGT  
CCACCAAGGGACGGGGCGTCTATGTGGGGCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG  
CCCTCATCGTGAGCCCTGAGCGAAGTGCTCACCTCACCAACAATGTCAACAAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGTCTGCA  
AGCTGCTGCGGCTGGATGACCTCTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCAGTGTCAACAAGACAGGGCACCAGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTCTTCATGGCACGGCTGGATGGAAGCAGGATTACTTCCGACCCCTGTCCA  
GCCGGAAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT  
TTTGTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCCACCTTGACAT  
CTTCTACATCTACGGCTTGTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA  
CCCTGAGGGTGTGCCATCAACTCCGCTGGAGACCTCTACACCTCACGATCGTCCGG  
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCTGCCCTGGCTGCACCCGGC  
CGGGGTGGAATACCGCCTCAGGCTGCTTACCTGCCAACGCTGGGACTCACTGGCCC  
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTGCCATCTCTCAAAGGGCAGAAG  
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTCCTCCCTATCCGGCCATCAACTT  
GCAGATCAAGGAGGCCCTGCAGTCCTGCTACCAAGGGCAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGAAGGACGCCAGTGCACGAAGGCCCTGCCCCATCGATGATAACTCTGTGGA  
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTGAGATGCTCCAATGCC  
ATTCACCTCTCAGCAAAGAGTCCCTTTGGAGGTAGCTATTGGTGGAGATTTAACTATAG  
GCAACTTATTTCTGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGTTAATTTGTG  
ACTTAGCTCTAGCTACTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA  
TTCAATATTCCTAACCTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKL TGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLAGSL  
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKI PSDLALVSHFDIFYIYGFASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRGVEYRLLQAAYLAKP  
GDSL AQA FNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGN  
LELNWLLGKD VQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTS VASYVYNG  
YSVVFGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEG SYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGGACTGGAGTGGAAACCGGGTCCCCCGCCTAGAGAACACCCGATGACCA  
CGTGGAGCCTCCGGCGGAGGCCGGCCCGCACCGCTGGACTCCCTGCTGGCTTGGCTCTGGCTCC  
GCAGGCTGGACTGGAGCACCCCTGGTCCCTGCGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGA  
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTCGGGGCTCCATCCACTATTCGTGTGCCAGGGAGTACT  
GGAGGGACCGCCTGCTGAAGATGAAGGCCTGGCTTGAAACACCCCTCACCACTATGTTCCGTGAAACCTGCATG  
AGCCAGAAAGAGGCAAATTGACTTCTCTGGAACCTGGACCTGGAGGCTTCGTCCTGATGGCCGAGAGATCG  
GGCTGTGGGTGATTCTCGCTCCAGGCCCTACATCTGCACTGAGATGGACCTCGGGGCTTGCCAGCTGGCTAC  
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTACCGAAGCAGTGGACCTTATTGACCAC  
TGATGTCAGGGTGGTGCACCTCCAGTACAAGCGTGGGGACCTATCATTGCGTGCAAGGTGGAGAATGAATATG  
GTTCCATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGAAACTGC  
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGACTTGGCCACCATCAACTTGCAGT  
CAACACACGAGCTGCAGCTACTGACCACCTTCTTCAACGTCCAGGGACTCAGCCCAGATGGTATGGAGT  
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCCTCACAAATATCTGGATTCTCTGAGGTTTGAAAACCGTGT  
CTGCAATTGTGGACGCCGCTCCATCAACCTCTACATGTTCCACGGAGGACCAACTTGGCTTCAATGAAATG  
GAGCATGCACTCCATGACTACAAGTCAGATGTCACCAAGCTATGACTATGATGCTGTGACAGAACGGCG  
ATTACACGGCAAGTACATGAAGCTCGAGACTTCTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG  
ACCTTCTTCCAAGATGCCGTATGAGCCCTAACGCCAGTCTGTACCTGCTCTGTGGACGCCCTCAAGTACC  
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGAAATGGACAGTCT  
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCTCAGTGGCACGTGATGTCAGGGCAGG  
TGTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTGGTGGAGATCGTGGCGAGTCAGTATGGGAGAATATTGATGACCAAGCGCAAAG  
GCTTAATTGAAATCTCTATCTGAATGATTCAACCTGAAAAACTTCAGAACTATAGCCTGGATATGAAGAAGA  
GCTTCTTCAGAGGTTGCCCTGGACAAATGGNNTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTGG  
TAGCTGTCCATCAGCTCACGCCCTGTGACACCTTCTGAAGCTGGAGGGTGGAGAAGGGGTTGTATTCA  
TCAATGCCAGAACCTTGACGTTACTGGAACATTGGACCCAGAACAGCTTACCTCCAGGTCCCTGGTTGA  
GCAGCGGAATCAACCAGGTACATTGAGGAGACGATGGCGGCCCTGCATTACAGTCAGGAAACCCCCC  
ACCTGGGCAGGAACCAGTACATTAGTGGAGGCTGGCACCCCTCTGCTGGGCCAGTGGAGACTGCCGCTC  
CTCTGACCTGAAGGCTGGCTGCTGCCACCCCTCACTGCAAAAGCATCTCTTAAGTAGCAACCTCAGGG  
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTAAACCTAAGCCTGCAGGAAAGGTGGATGGCTCTGGGCC  
TGGCTTGTGATGATGGCTTCTACAGGCCCTGCTTGTGCCAGGCTGTGGCTGTCTAGGGTGGAGC  
AGCTAATCAGATGCCAGCTTGGCCCTCAGAAAAGCTGCTGAAACAGTGCCTTGCACCCGACGTACAGCCC  
TGCGAGCATGCTGGACTCAGCGTGCTTGTGGCTTGGCCACATCCCTCATGGCCCCCAT  
TTTATCCCCGAATCCTGGGTGTGTCACAGTGTAGAGGGTGGGAAGGGTGTCTCACCTGAGCTGACTTTGTT  
CTTCCCTCACACCTCTGAGCCTTCTTGGATTCTGGAAGGAACCTGGCTGAGAACATGTGACTTCCCC  
TCCCTTCCCACTCGCTGCTTCCCACAGGGTGCAGGGCTGGAGAACAGAAATCCTCACCTGCGTCTCC  
CAAGTTAGCAGGTGTCTGGTGTCACTGAGGAGGACATGTGAGTCCTGGCAGAACCCATGGCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACCCATGGCCATGTCTGACATCC  
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACCCATGGCCATGTCTGACATCCAGGG  
GGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACCCATGGCCATGTCTGACATCCAGGGAGGAGG  
ACAGAACGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCGAACAGCAGGGCAGAGCAGCCCTCTTC  
GAAGTGTGTCAGTCCGATTGAGCCTTGTCTGGGCCCAGCCAAACACCTGGCTTGGCTACTGTCTGA  
GTTGCAGTAAAGCTATAACCTTGAATCACAA

## **FIGURE 64**

MTTWSLRRR PART LGLLLVVLGFLVLRRL DWSTLVPLRLRH RQLGLQAK GWNFM LEDST FW  
IFGGSIHYFRVPREYWRDRLLKMKACGLNT LTTYVPWNLHEPERGKFDFSGNLDLEAFVLM A  
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFT EAVDLYFDHLM SRVVPL Q  
YKRGGPIIAVQNEYGSYNKDPAYMPYVKKALEDRG IVELLLTSDNKDG LSKGIVQGV LAT  
INLQSTHELQ LTTFLFNVQGTQPKMVMEYWTGF DSWGGPHNILD SSEVLKTVSAIVDAG S  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVT SYDYDAVLTEAGDYTA K YMLRDFFGSISGIP  
LPPP P DLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVN GNGQSF GYI LY  
TSITSSGILSGHVHD RGQVFVNTVSIGFLDYKTTKIAVPLI QGYTVL RILVENRGRV NYGEN  
IDDQRKGLIGNLYLNDSPLKNFRIYS LDMKKSFFQRFGLDKWXSLP EPTLPAFFLG SLSIS  
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGCTAGCTAGGTGTAGGGTGGACGGTCCCAGGACC  
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGCTCGGCCGAGGCCCCCAGGACCTCATCTCCAATGTTGGAGGAATC  
CGACACGTGACGGCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC  
AAGAACGCTGTCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA  
GGCAGACACTCGGTGTTGCTAGTGGATAGGGTCATGACCGGTTCTCCTAGACGGGGCC  
CGTCCGCTATGTGTCTGGCAGCCTGCACTACTTCGGTACCGCGGGTCTTGGGCCGAC  
CGGCTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGACCTCATTGCCCTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTACATCTGTGCAGAG  
TGGGAGATGGGGGTCTCCCATCCTGGTTGCTCGAAAACCTGAAATTCATCTAAGAACCTC  
AGATCCAGACTTCCTGCCAGTGGACTCCTGGTTCAAGGTCTGCTGCCCAAGATATATC  
CATGGCTTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGTACATGAGGCACTTGGCTGGCTCTCCGTGCACTGCTAGG  
AGAAAAGATCTTGCTCTTACACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GACTCTATACCACTGTAGATTTGGCCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT  
CGGAAGTATGAACCCCATGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG  
AATGGTGCCGATAAGAAGGGACGCTTCCCTCCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCCACACCTAACGCTTTTGCTCTCGAGATGTCATCAGCAAGT  
TCCAGGAAGTTCTTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTTGGCATTACTGGCTTCTAGACTTGCTTGGCTTGGCCCCGTGGGCCAT  
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC  
GAACCTATATGACCCATACCAATTGGAGCCAACACCATTCTGGTGCCAAATAATGGAGTC  
CATGACCGTGCCTATGTGATGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG  
AGACAAACTATTTGACGGGAAACTGGGTCCAAACTGGATATCTTGGTAGGAGAACATGG  
GGAGGCTCAGCTTGGGTCTAACAGCAGTGAACCTAACGGCCTGTTGAAGCCACCAATTCTG  
GGGCAAACAATCCTACCCAGTGGATGATGTTCCCTGAAAATTGATAACCTTGTGAAGTG  
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCTTCTGGCCCCCACATTCT  
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGTTAACCTGGCCGGTACTGGACAAAGCAGGGCC  
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTCAACAAAATTA  
CATTGCTGGAACTAGAACGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGCACTGAAAGGTAGGCCGGCATGGTGGCTCATGC  
CTGTAATCCCAGCAGTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA  
CCAGCCTGGCCAACATGGTAAACCCCGTCTCCACTAAAAATACAAAATTAGCCGGCGTG  
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATTGCTTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTAAAAAAAAAA

## FIGURE 66

MAPKKLSCIRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGANISIQVENE  
YGSYRACDFSYMRHLAGLFALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGASVNMYMFHGGTNF  
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVPPLPPPSPKML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## **FIGURE 67**

GCTTGAAACACGTC TGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC  
ACCCACAATATGGCTTACATGTTAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACTTGAAGGAATATT  
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATTT  
GCGTTCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT  
CTTGTCAAGAGTTAGTGAAAATAAACCTAGGGAAATTAGTTGAACCATGAGTGGACATTG  
AAAAACTCAGGCAGCACATTCA CGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTAGCTTCTCGCGATCACTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTCAAAA  
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATT CATAATGACGGCAC  
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACCTGGAT  
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT  
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCTATTACCCATGTCA  
AAAACTTGGAGTCACTTATTCTCTAACACAACAGCTCGAACCTTACCAAGTGGCAGTATT  
AGTTACAGAAA ACTCAGATGCTTAGATGTGAGCTACAACAACATTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC  
CAAACAAATTGTTAAATGCATAAAGTTGAGGACTTTGAATCTGGACAGAACTGCATCACC  
TCACCTCCAGAGAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG  
TGGAAAGATCACCTTTGATAACCTGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCCTTGCAAATGGGATTTAAACTAAGATAATATATGACAGTGATGTGCAGGAAC  
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAATAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGTAGGGTTTAAGTCATTCACTTCAAATCATTGTTTTCTTTGGGG  
AAAGGGAAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACCTGGAT  
GCTGCCGCTACTGAATGTTACAAATTGCTGCCGTCAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRQHISRNAQDKQELHLFMLSG  
VPDAVFSDLTDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPA WVYLLKNLRELYLIGNLNSENNKMIGLESRLERLHLKILHVKSNLTKVPSN  
ITDVAPHLT KLVIHNDGT KLLVLNSLKKMMNVAEELQNCELERI P HAI F SLSNLQ ELDLKS  
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTI PPSITHVKNLESLYFSNNKLESLPVAVFSLQ  
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLSQLTQLELKGNCLDR LPAQLGQCRMLKKSGL VVEDHLFD TLPLEVKEALNQDINIP  
FANGI

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

**Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

**N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## FIGURE 69

CCACCGCGTCCGGCCTCTCTGGACTTGCAATTCCATTCTTTGACAAACTGACTTTTTATTC  
TTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCTGGGAAGACATTGTGTTTACACACATAAGGAT  
CTGTGTTGGGTTCTCTCTCCCCTGACATTGCATTGCTTAGGTACATCGAAGTCTTGACCTCCATACAGTATTGCTGTC  
GCTCAGTGCTTGCTGCACTTATCTGCCTAGGTACATCGAAGTCTTGACCTCCATACAGTATTGCTGTC  
ATCGCTGGTGGTACCTGCGGCCCTGCTCTGCTGATAGTTGTCGTCTGTCTTACTTCAAATACACAAC  
GCGCTAAAAGCTGCAAAGGAACCTGAAAGCTGTCGGCTGTAaaaaaaATACAACCCAGACAAAGGTGTGGTGGCCAAG  
AACAGCCAGGCCAAAACCATTGCCACGGAGCTTGCTGCGACATAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAA  
AGTTTGATTCCTGCCCCCTGCTGTCAGTAAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAA  
GCAGAGCCCTGAAAGACTTCAATGATGTCATGAGGGCACCTGTTGTGATGTCAGGACAGAAGAAAGGCACAG  
CTCCCCATCAGTTCATGAAAATAACTCAGTGCTGCTGGAAACAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGCAACCTTCAGGAAGGAGTTGGGGAGAGAGAACCCCTACTGTGGGAATGCTGATAAAACAGTCA  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGACTGACGTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCTATAAAAGCTGTCGGCTTAAGGCTGCCAGGCCCTGCAAAATGGAGCTTGT  
AGAAGGCTCATGCCATTGACCCCTTAATTCTCTGTTGGCGAGCTGACAATGGGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTCTAGGGGGTGCACATGGCAGAGACCCACAAGGCATGATCCTGCAACTCAATCCC  
AGTGAGAACTGCACCTGGACAATAGAAAGACAGAAAACAAAGCATCAGAATTATCTTCTATGTCCAGCTT  
GATCCAGATGGAAGCTGTAAGGATGAAACATTAAGTCTTGACGGAACCTCCAGCAATGGGCCTGCTAGGG  
CAAGTCTGCAGTAAAAGACTATGTCCTGATTTGAATCATCATCCAGTACATTGACGTTCAAATAGTTACT  
GAATCAGCAAGAATTCAAAGAACTGTCCTTGCTTCAACTACTTCTCTCTAACTATCTTCTATCCAAACTGT  
GGCGGTTACCTGGATACCTTGGAGGATCCTCACCAGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT  
TGTGTTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAACTCAAAGAGATTTCCTAGAAATAGAC  
AAACAGTGCATTTGATTTCTGCCATCTATGATGGCCCTCACCACACTGCTGCTGTTGCTACAGATTATGCCAATTCT  
GGCCGTGTGACTCCCACCTTCGAATCGTCATCAAACACTCTGACTGTCGTGTTGCTACAGATTATGCCAATTCT  
TACCGGGGATTTCTGCTCTCACACCTCAATTATGCAGAAAACATCAACACTACATCTTAACTTGTCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACACTAGAGGTTTAACTCTAATGGGAATAACTTGCAACTAAA  
GACCCAATTGCAAGACCAAAATTCAAATGTTGGAATTCTGCTCCCTTAAATGGATGTGGTACAATCAGA  
AAGGTTAGAAGATCAGTCATTACTACACCAATAATCACCTTCTGCTCCTCAACTCTGAAAGTGTGATCACC  
CGTCAGAAACAACTCCAGATTATTGTAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACAA  
GAAGATGATGTAATCAAAGTCAAATGCACTGGGAAATATAACACAGCATGGCTTTGAATCCAATTCA  
TTTGGAAAAGACTATACTTGAAATCACCATATTATGTTGGAACCAACTCTTGTGTCAGTTAGTCTGCAC  
ACCTCAGATCAAATTGGTGGTTCTGATACCTGTAAGGCCTCTCCACCTGACTTTGCATCTCCAAACC  
TACGACCTAATCAAGAGTGGATGTAAGTGTGAGATGAAACTTGTAAGGTGATCCCTTATTGGACACTATGGGAGA  
TTCCAGTTAATGCCCTTAAATTCTGAGAAGTATGAGCTGTGATCTGCACTGTAAGTTGATATGTGAT  
AGCAGTGGCACCACCAAGTCTGCTGCAATCAAGGTTGTCAGGAGAAGCAGACATTCTCATATAAATGG  
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATGCAAGTGCAAGTGGCAATTCAAGGATTCAGCAG  
GAAACACATGCCAAGAAACTCCAAACAGCCCTTCAACAGTGTGCACTGTTCTCATGGTCTAGCTG  
AATGTGGTACTGTAGCGACAATCACAGTGAGGCAATTGTAATCAACGGGAGACTACAAATACCAGAAGCTG  
CAGAACTATTAACTAACAGGTCAACCCCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTG  
GGCTACACATATTGAATAATGAGGAAGGGCCTGAAAGTGACACACAGGCCCTGATGAAAAAAA

# **FIGURE 70**

MELVRRLMPLTLIILSCLAEITMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIIFSIVQLDPDGSCESENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSSTLT  
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVGRVTPTFESSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVRSKRDISSYWKWKTDSIIGPIRLKRDRSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 71**

GACGGAAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATGCGGCCCCAGGAGCTCCCAGGCTCGCGTTCCCGTGTGCTGTTGCTGC  
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCCACGCCGCTCGACCCCACCTGGGAGTCC  
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCAAGTCGGCATCTCATCCACTG  
GGGAGTGTGTTCCGTGCCAGCTCGTAGCGAGTGGTCTGGGGTATTGGAAAAGGAAA  
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT  
TTTGGACCACTATTACAGCAAATTAAAAATTTTAATGCCAACAGTGGGCAGATATTTCAGGC  
CTCTGGTGCAAATACATTGTCTTAACCTCAAACATCATGAAGGCTTACCTGTGGGGT  
CAGAATATTGTGGAACGTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA  
ATGGTTTCACTCCGCTCTCCTGAGGATGAATCCAGTCATTCCATAAGCGGCAATTCCAG  
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG  
TCGGATGGTACGGAGGACCCGATCAAACTGGAACAGCACAGGCTCTGGCCTGGTT  
ATATAATGAAAGCCCAGTCCGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTCTACCTGCAGTGATCGTTATAACCCAGGACATTTGCCA  
CATAAATGGAAAATGCATGACAATAGACAAACTGTCTGGGCTATAGGAGGAAGCTGG  
AATCTCTGACTATCTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG  
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG  
GAGCGACTGAGGCAAGTGGGCTCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGCTATGCCATTAAATGGGCCACATCAGGACAGCTGTTCTGGCCAT  
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC  
GATTCTTGAGCAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC  
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACGGATAAGAAAATTATGGCAGTTCAAGCCCTTCCCTTTCCACTA  
AATTTTCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACTTGCCATTAAAGTC  
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTATGTTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT  
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTCCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAATACTGTAAAATGGTGCACCTGTATAGGGCACTTACCCAGGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA  
GTTTTCTTCTTCATTATAAACATAAGTGTACTGTAACTTACAAACGTTTAATT  
TTTAAACCTTTGGCTTTGTAATAACACTAGCTAAACATAACTCATTGTGCAA  
ATGTAA

## FIGURE 72

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHG  
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNTQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETY  
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

## **FIGURE 73**

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC  
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTCCATCTGGACCACGAGGCTCTGGCCAAGGCTTTGCCTGCAGAAGAGCT  
TTCCATCCAGGTGTCAAGCAGAATTATGGGGATCACCCCTGTGAGCAAAAGGCGAACAGC  
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAACATTGCAGCTATGGCTGGGTTGGAGA  
TGGATTCGTGGTCATCTCTAGGATTAGCCCCAACCCCAAGTGTGGAAAAATGGGGTGGGTG  
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT  
ACTTGGACTAACTCGTCATTCCAGAAATTATCACCAACAAAGATCCCATAATTCAACACTCA  
AACTGCAACACAAACAAACAGAATTATTGTCAAGTACACTACTCCTCCTGCTCCAGCTTCACTT  
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCACTTCACTTCCACGG  
AGAAAAAAATTGATTTGTGTCAAGAAGTTTATGGAAACTAGCACCATGTCTACAGAAC  
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTTCTCCTCTTGGTGTGAGCTGGCTTGGATTTC  
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTACAAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA  
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACCTACCGTGCATGCCTGGAA  
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC  
TTACCCCTGCCCTAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAAGAAAGTCCACCC  
GGTTCTTAACGGAAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAC  
CCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTCCCACGGCC  
TTCTAGCCTGGCTATGCTTAATAATATCCCACGGAGAAAGGAGTTTGCAAAGTGCAA  
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC  
CCTTCTCAGCTCTGAAAGAGAACACGTATCCCACCTGACATGTCCTCTGAGCCGGTA  
AGAGCAAAAGAACGGAGAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGTAAGCTAAAATAAAGAACAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTGCTCTGAACACATTGAGTTGGA  
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTCT  
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCACTAATTGTTAAAAAGTAATAAAATTCA  
ACAAACATTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCCTCAAAAATTGCACATAGTAGAACCGCTATCTGGGAAGCTATTCT  
GTTTGATATTCTAGCTTACTTCAACTTAACTTAAATTCTTAAACATACCTAACAGAAC  
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAACAGAAC  
TACATTGTTACCTCTATATACCAAAAGCACATTAAAAGTGCCTTAACAAATGTATCACTA  
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA  
AGCATTAGAAAATT

## **FIGURE 74**

MARCFSLVLLLTSIWTTRLLVQ GSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISP NPKCGKNGVGVLIW KVPVSRQF  
AA YCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP  
A PASTSIPRRKKLICVTEVF METSTMSTETEPF VENKA AFKNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP  
SKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 75

AGATGGCGGTCTTGGCACCTCAATTGCTCTCGTATTGGTGCACGACTTCACGATGG  
CTCGCCCAACCTTACTACCTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA  
ACTGCCGCCGCTCTGCCACGGCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAAACACAAT  
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACTAGAACGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTGCCAA  
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC  
GTACAGGGCTAAATTTGGGAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC  
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCTG  
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTTCAACCCCCACCACAGTGTCA  
TGGGAAAACAAGAAGGATAAAAGATCCTCACTTGGCAGTGCTCCTCTCCTGTCAATT  
CCAGGCTCTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG  
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGGATTGTCAG  
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGTCTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC  
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTTCTAG  
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA  
CGCTAAGAATTTCACCCAGGACTCTGCTTCAAGCCCTCTGGCTCGTTATGGTC  
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGTCCTAAGGAGAAACCTTAACCACAAAG  
TTTTTATCATTGAAGACAATATTGAACAACCCCCCTATTGTGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTCCCTTGTGGTAGGACTTGGAGGGAGAAATCCCTGGACTTCAC  
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT  
TCCTTTG

## FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRACKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## FIGURE 77

GGACAGCTCGGGCCCCCGAGAGCTCTAGCCGTCAGGGAGCTGCCCTGGGACGTTGCCCTG  
GGGCCCTGGCCGGGTACCCCTGGCATGAGGAGATGGCCTGTTGCTCTGGTCCA  
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTACAACGGCTTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCCGAGGGAGACCCCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCTGGTCTCCCAGGGCGTGTGCGTGTCAAATGGTGGAAAGCT  
GTCGGAGAACGGGCCAGAGAAGGACGTGCTGGTGCCATGGGCTGAGGCACCGCTCCT  
TTGGGACTACCAAGGCCGCGTGCACCTGGCAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGA  
GGATGAAAGCGGTCTGGTGAGGACTGGAGCTGGAGCTGCGGGGTGTGGTCTTCCTTACCA  
ACGGCGCTACCAAGTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCC  
GTGGCCTCCTTGAGCAGCTCTCCGGGCTGGAGGAGGGCTGGACTGGTGCAACGCC  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCC  
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCCTGCACCGCTATGAT  
GTATTCTGCTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCCTGAGAAC  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC  
AGCTCTTGCCGCTGGAAGTCCATGCCCTGGACCGCTGCCACGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCCGTGGTTACCCGCATCCTAACTGTGGCCCCCAGAGCCTGGG  
CCGAAGCTTGCGCTCCCCGACCCGCAGAGCCGTTGTACGGTGTACTGCTACGCCAGC  
ACTAGGACCTGGGCCCTCCCGGCCGCATTCCCTCACTGGCTGTATTATTGAGTGGTT  
CGTTTCCCTGTGGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTTCT  
TTAAACATTTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTCCCTGCTCCTG  
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGCCATTGCGGTTGTGGCTTCTG  
GAGGGTCCCCGCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGGTGGCCAGAGTGGC  
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTTCTCCCTGCC  
CAGCCTGGGGAAAGAAGAGGGCCTGGGGGCTCCGGAGCTGGCTTGGCCTCTCCTGCC  
CACCTCTACTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTCAGGCAGAACATCTGAGGAAAGAAACTCCCTCCCCGTTCC  
TCCCTCTCGGTTCAAAGAACATGTTGTCATTGTTCTCCTGTTCCCTGTGTGG  
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGTATGACTGCCCTCGCCAA  
AA  
AA

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFVQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSGPR  
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## FIGURE 79

## **FIGURE 80**

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ  
FRDFRDLNKDGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

## **FIGURE 81**

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGC GGAGCCCCGG  
GCGGCAGGGCGCGGGTGCAGGGGATCCCTGACGCCCTGTGCCCCTTTGTCGCTCCAG  
CCTGTCGTCGTCGTTGGCGCCCCCGCCTCCCCCGGGTGCAGGGGTTGCACACCGATCCTG  
GGCTTCGCTCGATTGGCGCCGAGGGCGCTCCCAGACCTAGAGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCGTCGTCCTCTCCCTCGCGCCGCCGGGATCCGAAGGGTGCAGGGGCTCT  
GAGGAGGTGACCGCGGGGCTCCCAGCACCTGGCCTGCCCCTGAGCAGGGTGCAGGGGCTCT  
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCAGCTCGGCCTCGGTGTG  
TGTCTGCTGCTGCCGGGCCCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG  
TTTACCAAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGCTGCC  
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTCTGTATCGAGCATATGTGGG  
GCTGCTGTCACAGGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAACATTCTCAGTAGATGCCATGGCATCCAGTCTCAAATGCTTCTAGAT  
GGTCTGCTCTTCACAGTAACAAAGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCAGAAGAAAAC  
CAATAAAGATTGTAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC  
GCCGATTTAACATTACAGAAGAATTGGCTTAATGTTGGAAAGTGGCTCTAACATTGGAA  
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA  
AAACTTACATCAGCAAAGATGTTGTTGCCATAAGGAAGTAGGTTAGGGCTAGAGGGGTA  
ATTCCAATACAGGAAAAGCCTGAAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA  
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT  
CGGAATAATGGCTTCTCTTACCATGCCAACTGGTTGGCACCAAAATACGTAAA  
GCCTCTGGTACAGAACGCTGTGCACTCATGAACAAATGATGTGCAAGACCTGTTATAACT  
CAGTGAACATTGCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCCTC  
ATGCTGAAATTGTTCCAACATAGCCAAGACTTTGAAATCTCGGACATTGGTCCAAGAT  
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA  
AAGAGAATGTCCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT  
GATGCCATTCTTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA  
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTCTGTGGTGGCTGGCACCTCTGGATGACCTG  
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTCACAAGAGAGTTCACAGGATT  
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTTAGAGATTCTTACAATCCCAGCAAT  
AATGGTAACATTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAATTGTATT  
CTCATAACTGAAATGCTTACTGATGACATAGAATCAGATAACAAACTATTAAGTATGTCAAC  
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT  
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA  
TTCCATAGCTCAATAAAAGAATCTGATACCTTAGACCAAAAAAA

## FIGURE 82

MSAAWIPALGLGVCLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPPEKKTGNKDKCKADIAFLIDGSFNIQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSSDIEEAGIVAREFGVNFIIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI  
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLA  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

## **FIGURE 83**

CGCCCGCGCTCCCGCACCGCGGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC  
GGCGGCCTCCCGCGGGAGCGAGCAGATCCAGTCCGGCCCGAGCGCAACTCGGCCAGTC  
GGCGCGGGCTGCGGGCGCAGAGCGGAGATGAGCGGGCTGGGGCACCCCTGCTGTGCCTGC  
TGCTGGCGGGCGGCGGTCCCCACGGCCCCCGCCGCTCCGACGGCGACCTCGGCTCCAGTC  
AAGCCCGGCCCGGCTCTCAGCTACCCGAGGAGGACACCGCAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG  
GGTTGAGGAAGTGTGAGGACACGCAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG  
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACACTACCTCCAGCTAT  
ACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACAACAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGCGAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC  
ATGTACTGCCAGTTGCCAGCTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT  
CTGCACCCGGGACACTGAGTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA  
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG  
TGCTGTGCCTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA  
GCTTGCATGACCCGCCAGCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG  
GAGCCTGGACCGATGCCCTGTGCCAGTGGCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCACCTCGTGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGTGCCGCT  
GCACTGCTGGAGGGAAAGAGATTAGATCTGGACCAAGGCTGTGGTAGATGTGCAATAGAA  
ATAGCTAATTATTCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTCCTACA  
TCTTCTCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGCAATTGTTCA  
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCTTGGGAGAGTCAGGCAGGGTTAAC  
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACAGTTGGCAG  
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG  
AGTCTCCCTGTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA  
CCTGGCAAAATGCAACAAATGAATTTCACCGAGTCTTCCATGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCTGCATTACATGTGTTATTCA  
AGCAGTGTGCTCAGCTCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT  
CCTCTCTCAGCACAGCCTGGGGAGGGGTATTGTTCTCGCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCA  
CTGGTTGTGACTCTAAGCTCAGTGCTCTCCACTACCCACACCAGCCTGGTGCCACCAA  
AAGTGTCCCCAAAAGGAAGGAGAATGGGATTGGGACTTGAGGCATGCACATCTGGAATTAA  
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC  
AGTGTGGGGAGCCGCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTGGCAGT  
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATAACAGTTAACCTGCAGAAACA  
GTACTTAGGTAATTGAGGGGAGGATTATAAATGAAATTGCAAAATCACTAGCAGCAAC  
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT  
GTAATATGCGACTGCCAACATGTATTGACACTGCTACGCCACTCCACAAATGATGTTTCA  
TGGACTGTTGCCACCATGTATTGACACTGCTTAAAGTTAAAGTTGACATGATTGTA  
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTGCATTAGAAATCAAGC  
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

600 700 800 900 1000 1100 1200

## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDTKGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPCASGLLCOPHSHLVYVCKPTFVGSRDQDGIELLPREVPEYEV  
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGEEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 85**

AAGGAGGGCTGGGAGGAAAGAGGTAAGAAAGGTAGAGAACCTACCTCACATCTCTCTGGGCTCAGAAGGACTCTG  
AAGATAACAATAATTCAAGCCCATCCACTCTCCTTCCCAAACACACATGTGCATGTACACACACATACA  
CACACATACACCTTCCTCTCCTCACTGAAGACTCACAGTCACTCACTCTGAGCAGGTCATAGAAAAGGACAC  
TAAAGCCTTAAGGACAGGCCATTACCTCTGAGCTCTGGCTTGAGTCAGGAAACATGGAGGG  
CCAGGCACGGTACTCACACCTGTAATCCCAGCATTGGAGACCGAGGTGAGCAGATCACTTGAGGTCAAGGAG  
TTCGAGACCAGCCTGGCCAACATGGAGAAACCCCCATCTCACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC  
AGGTGCTGTAATCCCAGTACTCAGGTGGCTGAGCCAGGAGAATCGCTGAATCCAGGAGGGAGGATGCCAGT  
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGTGCAGAATGAGACTCTGTCTCAAACAAACACGGGAGGA  
GGGTAGATACTGCTTCTGCAACCTCCTAACCTGCACTCTGATCTTCCAGGGCTGCCCTGATGGGCCCTG  
GCAATGACTGAGCAGGCCAGCCCCAGGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGA  
GTGAGAATGACTGCCCTGGGAGGGTGGTCTTGGGCCCTGGCAGGGTTGCTGACCCCTAACCTGCAAAACAC  
AAGAGCAGGACTCCAGACTCTCCTGTGAATGGTCCCTGCCCTGAGCTCCACCAATGAGGCTTCTCGTGGCCCC  
ACTCTTGCTAGCTGGGGCTGGTGCCTGCACTGTGCCACTGTGCCCTGGTACCCGGATGTTCCCTGCCCTCA  
GTGTGCTGCCAGATCCGGCCCTGGTATACGGCCCTGCTGCTTACCGCGAGGCTACCACTGTGGACTGCAATGA  
CCTATTCTGACGCCAGTCCCCCGGCACTCCCCGAGGCACACAGACCCCTGCTGAGGCAACAGCATTGT  
CCGTGTGGACCAGAGTGAAGTGGCTACCTGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTGGA  
TGCCCGAGACTGTGATTCCATGCCCTGCCCTGGCAGCTGCTGAGCCTGACCTAGAGGAGAACCGAGCTGAC  
GGAGGACACAGCTTGCAAGGGCTGGCAGGCTACAGGAACACTATCTCAACCACAACCAGCTTACCGCATCG  
CCCCAGGGCCTTCTGGCTCAGCAACTTGTGCGGCTGCACCTCAACTCCAACCTCTGAGGGCCATTGACAG  
CCGCTGGTTGAAATGCTGCCAACTGGAGACTCATGATTGGGGCAACAAGGTAGATGCCATCCTGGACAT  
GAACCTCCGGCCCTGGCCAACCTGCGTAGCCTGGTCTAGCAGGATGAACCTGCCGGAGATCTCGACTATGC  
CTTGAGGGCTGCAAAGCCTGGAGAGCCTCTTCTATGACAACCAGCTGCCCTGGGTGCCAGGCGGGCACT  
GGAACAGGTGCCGGCTCAAGTCTCTAGACCTCAACAAGAACCCGCTCCAGGGTAGGGCCGGGACTTGC  
CAACATGCTGACCTTAAGGAGCTGGACTGAACAACATGGAGGAGCTGGTCTCCATGACAAGTTGCCCTGGT  
GAACCTCCCCGAGCTGACCAAGCTGGACATCCAATAACCCACGGCTGTCTTCTATCCACCCCCGGCCTTCA  
CCACCTGCCCTGGAGGACCTCATGCTCAACAACACGCTCTCAGTGCCTTGACCCAGCAGACGGTGGAGTC  
CTTGCCCAACCTGCAAGGGTAGGTCTCACGCCAACCCATCCGCTGTGACTGTGTCATCCGCTGGCCAATGC  
CACGGGCACCCGTGTCGCTTATCGAGCCGAATCCACCCCTGTGCGGAGGCTCCGGACCTCCAGCGCCTCCC  
GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCAACTGTTGCCCTCATCTCCCCAGAAGCTTCCCCCAAG  
CCTCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACTGCCGAACCCGAACCCGAGATCTACTG  
GGTCACTCCAGCTGGCTCGACTGACACCTGCCATGCAGGCAAGGAGGTACGGGTGACCCGGGACCT  
GGAGCTGCGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTTGGCCAGAACCTGGTGGGGCTGACAC  
TAAGACGGTTAGTGTGGTGTGCGCTCCTCCAGCCAGGAGGGCAAGGACAGGGGCTGGAGCTCC  
GGTGCAGGAGACCCACCCCTATCACATCTGCTATCTGGTCAACCCACCAACAGTGTCCACCAACCTCAC  
CTGGTCCAGTGCCTCCTCCCTGGGGCCAGGGGCCACAGCTGGCCCTGCCTGGGGAAACCCACAGCTA  
CAACATTACCGCCTCCTCAGGCCACGGAGTACTGGGCTGCCGCAAGTGGCTTGTGATGCCACACCCA  
GTTGGCTTGTGATGGGCCAGGACCAAAGAGGCCACTCTTGCCACAGAGCCTAGGGGATGTCCTGGCTCAT  
TGCCATCCTGGCTCGCTGCTCTCTGGCAGCTGGCTAGGGCCACCTTGGCACAGGCCAACCCAGGAA  
GGGTGTGGGTGGGAGGCGCCTCTCCAGCCTGGCTTCTGGGCTGGAGTGGCCCTTGTCCGGGTTGT  
GTCTGCTCCCTCGTCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC  
ACCATTGTCTAAATTCTTGAAGCTCAGCCTGCCAGGAAAGGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGC  
CAAGACAGATGGGCTTGTGGCCCTGGGGGCTCTGAGCCTGGCTTCTGAGCCTTGGCTTACCTCCTAGGGTCA  
CCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGGAGGGACTTGGCTAGAGCCTCCCTGCCCTCCCCATCTT  
CTCTGCCCCAGGGCTCTGGGCCCTGGCTTCTGCTTCTGCTTCTGCTGCCCTGGCTGCAACCCCTTCTCTTC  
TCTTCTCTGTAAGTCTCAGTTGCTTGCTTCTGCTTCTGCTGCCCTGGCAAGGGCTGAAGGAGGGCACTCCATCTCAC  
CTCGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAA  
CGCCTCATCTCAGCAGCCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGCAATTGGTACCTTGTGGAGAA  
ATGTGTCACCTCCCCAACCGATTCACTCTTCTCTGTTGAAAAAATAAAATAACAATAAAA  
AAAA

100 200 300 400 500 600 700 800 900

## FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCCNDLFLTA  
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQEELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSILVLAGMNLREISDYALEGLQSLESLSFYDNQ  
LARVPRRALEQVPGLKFLDLINKPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP  
ELTKLDITNNPRLSFIHPRAFHHLQPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDQLQRLPVREVPFREMTHCLPLISPRSFPSSQ  
VASGESMVVLHCRALAEPEPEIYWVTPAGLRLTPAHGRRYRVYPEGTLELRRVTAAEAGLYT  
CVAQNLVGADETKTVVVGRALLQPGRLDEGQGLELRVQETHPYHILLSWTPPNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVALLLAAGLA AHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV  
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## FIGURE 87

GCAAGGCCAAGGCCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGGGGACATTGTGTACCGCCT  
CTACATGGCGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTGACGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC  
CCTGGCACACTCTCAAGATCCTGGCTCCTCATACATCAGCCTAGTCATCTTACGGCCTCATCTGCATGTA  
CACACTGTGGTGGATGCTACGGCCTCCCTCAAGAAGTACTCGTTGAGTCGATCGTGGAGGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAACGACTTCGCCTCATGCTGACCTCATTGACCAATACGACCCGCTACTCCAA  
GCGCTTCGCCGTCTCTGTGGAGGTGAGTGAGAACAGCTGGCAGCTGAACCTCAACAACGAGTGGACGCT  
GGACAAGCTCCGGCAGCGGCTACCAAGAACGCGCAGGACAAGCTGGAGCTGACCTGTTCATGTCAGTGGCATT  
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCCCTAAGCTGGAGCTGATCCCGACGTGACCATCCC  
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGGCTCTACACACAGCGGCCAAGATTGAAAGCGCTGCGCT  
GGCCTTCTGCGCGAGAACCTGCGGGCCTGCACATCAAGTTACCGACATCAAGGAGATCCGCTGTGGATCTA  
TAGCCTGAAAGACACTGGAGGAGCTGACCTGACGGCAACCTGAGCGCGGAGAACAAACGCTACATGTCATCGA  
CGGGCTGCGGGAGCTCAAACGCCCTCAAGGTGCTGCCAGCTCAAGAGCAACCTAACGAAAGCTGCCACAG  
AGATGTGGGCGTGCACCTGCGAGAACGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAG  
GAAGATGGCGAACCTGACTGGAGCTGATCCGCTGCGACCTGGAGGCGATCCCCCACTCCATCTCAGCCT  
CCACAACCTGCGAGAGATTGACCTCAAGGACAACAAACCTCAAGGACCATCGAGGGAGATCATCAG  
CTTCCAGCACCTGCACCCCTCACTCCCTTAAGCTGTGTAACACACATGCCCTACATCCCCATCCAGATCG  
CCTGGAGCGCCTCTACCTGAAACCGCAACAAGATCGAGAACGATCCCCCAGCTCTTACTGCCAGCTGC  
CTACCTGGACCTCAGCCACAACAAACCTGACCTTCCCTGCCAGATCGGCCCTCTGCGAGAACCTCCAGAAC  
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCGGAGCTTCCAGTGCCGGAAGCTGCCGGCCCTGCAC  
GGGCAACAAACGTGTCAGTCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACCGAGATCGAGCTGC  
CAACCGCTGGAGTGCTGCTGTGGAGCTGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTGGTGGAGGA  
GGACCTGTTCAACACACTGCCACCCAGGTGAAGGAGCGCTGTGGAGGGCTGACAAGGAGCAGGCCTGAG  
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGAGGGCAGGCCTAGCTTCTCCAG  
AACTCCCGGACAGCCAGGACAGCCTCGGGCTGGCAGGAGCCTGGGGCCGTTGTGAGTCAGGCCAGAGCAGA  
GGACAGTATCTGTGGGCTGCCCTTTCTCCCTCTGAGACTCACGCCAGGGCAAGTGCTTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGCTCTCCCTGGAGGCCAGCTGCCAGGGCTGAG  
CTGCCACCAGAGGTCTGGGACCCCTACTTAGTTCTGGTATTATTCTCCATCTCCACCTCCTCATCC  
AGATAACTTATACATCCCAAGAAAGTCAGCCCAGATGGAAGGTGTCAGGGAAAGGTGGCTGCC  
TTGTCCCTTATTAGCGATGCCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGCCGGGGCAAC  
CCATGGGACGGTCAACCAGCAGTGCCGGCTGGCTCTGCGGTGCGGCCAGGGCCTCCAGCTGG  
AAGGCCAGGCCCTGGAGCTTGCTCTCAGTTTGAGCTTGTGGCAGTTAGTTTTGT  
AAACAATTTTAAAAAAAGCTTGGAAAATGGATGGTTGGGTATTAAAAAGAAAAAAACTTAAAAAA  
AAAAGACACTAACGGCCAGTGAAGTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAG  
TGAACGTGTTCTTCCCTGGGCCAGGGTGCAGGGTGTCTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT  
CTATTGTTCTGGGGAGGGAGGTTTTGTGTTGGTTGGGTTTTGGTGTCTGTGTTCTTCTCCTCC  
ATGTGTCCTGGCAGGCCACTATTCTGTCGGCTGGGCCAGAGGGAAATGTTCTGGAGCTGCC  
ACTCGGGTGGCTAATCCCCGATGAAACGGTCTCCATTGCCACCTCCCTCTGCCCTGCC  
CGCACAGTGTAAAGGAGCCAAGAGGAGGCCACTTCCGGCAGACTTGTGTTCC  
CCAGTGCCACCGCTGGCCTCCGCTGTTCCATCAGCCCTGCGCACCTGGCTCT  
GAGGCTGGCGGAAAGGGAGGTCGCCCTGGGAGGGCAGGCCGTTGGTCAAGCG  
CTGGAGTGACACAGCCAGTCGGCACCTGGTGGCTGGAGGCCAACCTGCTT  
AGATCACTCGGTCCCCACCTT  
AGAAGGGTCCCCGCCCTAGATCAATCAGTGGACACTAAGGCACGTTTAGAGTCTTGTCTTA  
CCATCCGTCTGTCGCTCCATTGTGTTCTGCGTGTGTCATTGGATATAATCCTCAG  
CCTCTGACAACCATGAAGCAAAATCCGTTACATGTGGGTCTGA  
ACTTGTAGACTCGGTACAGTATCAAATAA  
ATCTATAACAGAAAAAAAAAAAAAA

## FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIFKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRLQLNNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFSDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFDTIKEIPLWI  
YSLKTLEELHLTGNLSAENNRIVIDGLRELKRLKVLRLKSNLSPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ  
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNVLQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCCGCTGCTGGCCTGAACGCAGGAGCTGTCATTGACT  
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACCTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTTGGAAACTTGAGGAAATTGGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT  
GTGGATAATCCC GTGGCACTGGTT CAGTT ATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG  
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGT CCTATGGAGGAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTTATAAGGCCATT CAGCGAGGGACC ATCAAGTGC AACTT GCGGGGT  
TGCCTGGGTGATT CCTGGATCTCCCTGTTGATT CGGTGCTCTCCTGGGACCTTACCTGT  
ACAGCATG TCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTG CAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTA ACTAAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCTAGAATT CACACAGAGGCCACCTAGTTGTCTTGTCAGCGC  
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGCCCATCAGAAAGAA  
GCTAAAATTATTCTGAGGATCAAT CCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGT CAGGAGGCCTG  
GGTGC GAAACTGAAGTGGCCAGAACTGCCTAAATT CAGTCAGCTGAAGTGGAGGCCCTGT  
ACAGTGACCC TAAATCTTGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCATATGGT CTTCTGACCAAGGGACATGGCTCTGAAGAT  
GATGAGACTGGT GACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT  
AACTGGGCTGTGATCAAGAACGGTTCTGACCA GCTTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTGGAAATTATTCTGCTCTAAAAAAACCTAAGATTTTAAAAAATTGAT  
TTGTTTGATCAAAATAAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLLP<sub>1</sub>LLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE  
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCAGCGCCGTTATCAGGACCATGCAGGCCGA  
CGGGTCATCACGTGCGCAGCGTGGGAGAGGACGCCGAACCTGGCGTTGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTCGTATCGAATATCTATCTGAGCCCTCGTACCTGGGAATTCACCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTACCTACACTAAACACATCCAGCCCCTGTCTCCAG  
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCAGTGCATCTCCCCACACCCTCCAGGAAGTTCAAGGTGCCATCATAAACAA  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG  
GTTTGTGCTGGCAACGCCAACGGCGGAAGGATGCCTGCTCGGTGACTCAGGTGGACCCCT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG  
GTCGGCCAATCGGCCGGTGTCTACACCAATATCAGCCACCACCTTGAGTGGATCCAGAAG  
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGCCACTACTCTTTCCCTCT  
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGC  
CACTGCCAAGTCAGGCCCTGGTCTCTGTCTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLALLARAGLRKPESQEAPLSGPCGRRVITSRIVGGEDAELGRWPQGSLRLW  
DSHVCVGVSLLSHRWALTAAHCFETYSIDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTAKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## **FIGURE 93**

CCCACGCGTCCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCCTAGGGCT  
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCAGGCCGACCAGCGAGGACGC  
TGCCCCCAGGCTGGGTGCCCCCTGGCGTGCAGGACCCCTGAGGAAGAGCTGAGTCACCTT  
GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCGGATCCCAG  
CTCTCCTCAATAACGGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTGGCCATCCC  
CACTGACCCCTCCACACGGTGCAGGGAAATGGCTCTGGCAGCCGGAGGCCAGAAGTGCATTCT  
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATTGACAAGCAGAGCTGCTGCTCCC  
TGGGCTGAGTTCATCACTATGTGGGAGGACCTACGAAACCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTGTGGGGGACTGCACCGT  
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGGTAACCCCTGTGATCCGTAAGCGATACAACCTGACCTACAAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTCCATGAC  
TCAGACCTGGCTCAGTCATGCGCCTTCTGGCAACTTGACATCAGGCATCAGTAGC  
CCGTGTGGTGGACAACAGGGCCGGGGCCGGGATTGAGGCCAGTCTAGATGTGAGT  
ACCTGATGAGTGCTGGTGCACATCTCACCTGGGCTACAGTAGCCCTGGCCGGCATGAG  
GGACAGGAGCCCTTCCTGCAGTGGCTATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGGCCTACATCCAGCGGGTCA  
ACACTGAGCTCATGAAGGCTGCCGCTGGGTCTCACCTGCTCTCGCCTCAGGTGACAGT  
GGGGCCGGGTGGTCTGTCTGGAAAGACACCAGTTCCGCCAACCTTCCCTGCCTCCAG  
CCCCTATGTCACCACAGTGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA  
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTCATACCAGGAG  
GAAGCTGTAACGAAGTTCTGAGCTAGCCCCCACCTGCCACCATCCAGTTACTTCAATGC  
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTGATGGCTACTGGGTGGTCAGCAACA  
GAGTGCCATTCCATGGGTGTCGGAACCTCGCCTCTACTCCAGTGGTTGGGGGATCCTA  
TCCTTGATCAATGAGCACAGGATCCTAGTGGCCGCCCCCTTGGCTTCTCAACCCAAG  
GCTCTACCAGCAGCATGGGCAGGTCTTGTGTAACCCGTGGCTGCCATGAGTCCTGTC  
TGGATGAAGAGGTAGAGGGCAGGGTTCTGCTCTGGCTGGTGGATCCTGTAACAGGC  
TGGGGAACACCAACTCCCAGCTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCTATC  
AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTATTCTGCCCTGTG  
GAAGCCCTGCTGAACCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA  
TGCTGTGAGCTTGACTTCACTCCACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGATGCCCTCCCTCCGC  
ATCTCATCTTCTCTTCAATCAGGTTTCAAAGGGTTGTATACAGACTCTGTGCACTA  
TTCACTTGATATTCAATTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT  
TTCCTACCTGACATCCAGAAACAATGGCCTCCAGTGCATACTCTCAATCTTGTGTTATG  
GCCTTCCATCATAGTTGCCACTCCCTCTCCTACTTAGCTCCAGGTCTTAACCTCTG  
ACTACTCTTGTCTTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTCATTG  
TCCATTGAGATTGGCTCTCAGTTACTCATTGCCCCGGAACAAATCACTGACA  
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATAACCTCAA  
TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSITFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAELLPGAEFHYYVGGPTETHVVRSRSPHYQLPQALAPHVDFVGGLHRFPPSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYILMSAGANISTWVYSSPGRHEGQEFLQWLML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHECLDEEVEGQGFCSGPWDPVTGWGTPTSQLC

**Signal sequence:**

amino acids 1-16

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

**N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## **FIGURE 95**

GCCGCGCGCTCTCTCCGGCGCCCACACCTGTCTGAGCGGCGAGCGAGCCGCCGGC  
GGGCTGCTCGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTCCTTC  
TTCTTCTGCTCTGTGCTGTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG  
GCCTGCATAACCGCCTCCCTGCGTCTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT  
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTAAGGGAACCT  
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG  
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC  
ACCGAGACTCAGGGCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC  
AGGTTCAGCATTGGAAAGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACGATGTCCACAGCTGCCACTGCA  
TACACGATGAAAAAACCTATGTGAAAGGAACCCAGAACGCTTCAGTGGCTTCTAAAGCCC  
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA  
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACTCAAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGGTGAGCCCTCTGCTAACGAGCTGCCAGGGGCCAGAACATTCACTTCTC  
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA  
CCTATGACTGCTCTACCAGCAATGCCATGCCAGCCAGGGGCCAGGGCTGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAACGTTGGAGCCAAAAATTATTGGCATTTCAGG  
GCACCAGTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC  
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG  
TGACACAGTGGCCCTGGCAGCAATTAGGGCTTCATGTTCTTATTTAGGAGAGGCC  
AAATTGTTTGTCAATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATG  
GTTTGTGTATCATATCATATCATTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA  
AAAAAAATCTGATTGGGGCAATGAGGAATATTGACAATTAGTTAATCTCACGTTTG  
CAAACTTGATTTATTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA  
CAAGAGATATGAAAAAAAAAAAAAA

## **FIGURE 96**

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA  
KPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD  
SGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTA  
AHCIDHGKTYVKG  
TQKLRVGFLKPDKFDGGRGANDSTSAMPEQMFKQWIRVKRTHVPKGWI  
KGNANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDV  
KDETYDLYQQCD  
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAV  
RITPLKYAQICYW  
IKGNYLDCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## FIGURE 97

GCATGCCCTGGGTCTCTGAGCCTGCTGCCCTGCTCCCCGCCCCACCAGCCATGGTGGTT  
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTGGCACCTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC  
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATAACCTGTTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCCTGGCTCTGGTCCCAGAACGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCCGTGTATT CCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCCGCCATCTGCCAACCTGATGCCCTATCCACCT  
CCCTCCAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTG  
CCCACCCCTCAGACCCCTGCAGAACGCTGAAGGTTCTATCATGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT  
GGAGGGGGAGCAGGGATGCTTGTCTGGCGACTCCGGGGCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGCGAGGGCTGTGCCAGCGAACAGGCC  
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGTGGAGAACGATCGCAAGGGTGCA  
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCC  
CCGCGCGCTCCTAGGGCGCAGCGGACGCGGGCTCGGATCTGAAAGCGGCCAGATCCACA  
TCTGGATCTGGATCTGGCGGCCCTGGCGGTTCCCCCGCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCGGACGGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC  
GGCCTCAGGCCCCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAAC  
GACTTCCGGCCCCGCCGGGGCCCCAGCGCTTTGTGTATATAAATGTTAATGATT TATT  
AGGTATTGTAACCCCTGCCACATATCTTATTATTCTCCAATTCAATAAATTATTATT  
CTCCAAAAAAA

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWVITAHCFKDNLNKPYLF SVLLGAWQLGNPGSRSQKVGVVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC  
QVDGAWLLAGII SWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSGQ  
SGAAARS

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 99**

GACGGCTGCCACCAATGCACGGCTCCTGAGTTCTGATGCTCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGGCCCAGGTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCTTCGCCAAGGCCTACGCACGGCAGTGCAGTGGGGCAC  
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT  
GCAGCCCAGGCCAGATGTGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC  
GGCTGTGGTCCCACCTCTGTGAGAAAGCTCCAGGGTGGTGGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGAAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC  
CGTGCCTCCAAATGTCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTGCTTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC  
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCACCTGCGTAAC  
AACTGAGGTCCCTTCCATTGGCAGCTCACAGCCTGCCCTCCTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTCCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGGCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGCAAG  
GGAACCTCCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTCCAGTG  
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGCTTGCCAGGTGCAGAGGCCCTGACA  
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGGCCCTGGCATGTGTGGGCCCTCCTGGGA  
CTACTGCTCCTGCCTCCTCTGGTGGCTGGAATCTTCTGAATGGGATACCAACTCAAAGGG  
TGAAGAGGTCAGCTGTCCCTGTCATCTTCCCCACCCGTCCCCAGGCCCTAAACAAGATA  
CTTCTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCCTCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC  
GGGCCACACCTCTCCTGCCCTCCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG  
TGTAGCTGGGGATGGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTC  
TTTGAGTGGGGAGGCAGGGACGAGGAAGTAACTCCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAAA

Figure 99

## **FIGURE 100**

MHGSCSFLMLLLPLLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPASDMILHMRWDEE  
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMVDPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGRPYQEGETPCSQC  
PSGYHCKNSLCEPIGSPEADAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHLPSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNSGPGHVWGPLLGLLLLPPVLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

## FIGURE 101

GTAACGTGAGTCAGGGCTTTCATTTGGGAAGCCCCCTCAACAGAACCGGTCAATTCTCCAAGTTATGGTGGACGT  
ACTTCTGTTGTCCTCCCTGCTTGCTTTACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTTCAT  
CAAGGCAAGTCCATGAGCCACCTTCAAAGCCTCGAGAACTGAACAACAATGAATTGGAGACCATTCC  
AAATCTGGGACCAGTCTCGGCAAATATTACACTTCTCTCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA  
ACATCTGAAAGAGTTCACTGAAACTTTGGACCTAGCAGAACAAATATTCAAGAGCTCCAAACTGCATT  
TCCAGCCCTACAGCTCAAATATCTGTATCTCACAGAACCGAGTCACATCAATGGAACCTGGGTATTTGACAA  
TTTGGCCAACACACTCCTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACT  
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTAAAATGTAGATGGACTGACATTCCAAGGCCTGG  
TGCTCTGAAAGTCTCTGAAATGCAAGAACAGGAAACTTATGGATGGAGCTTTGGGGCTGAGCAA  
CATGGAAATTTCGAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCT  
GCAGGAACCTCATCTCAGCCAAAATGCCATCACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAAGCTCAG  
TGAGCTGGACCTAACTTCACTTCAAGGTTAGATGATTCAAGCTTCTGGCCAAGCTTACTAAATAC  
ACTGCACATTGGAACAAACAGACTCAGTCATTGCTGATTGCTCTCCGGGGCTTCCAGTTAAAGACTTT  
GGATCTGAAGAACAAATGAAATTCTGGACTATTGAGACATGAAGACATGGTCTTCTCTGGGCTTGACAAACTGAG  
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTTACTAAAAAGCCTTACTGGTTGGATGCAATTGGAGCA  
TCTAGACCTGAGTGACAACGCAATCATGTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATT  
GCATTAAATACATCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCACAGGGGGGGAAAACAACTT  
TCAGAGCTTGTAAATGCCAGTTGTGCTGCCCCATCCTCAGCTGCTAAAGGAAGAACGATTGGCTGTTAGGCCAGA  
TGGCTTGTGTTGATGATTCCAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTT  
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTGCTGGAAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGAAATTATGCACACCTCCGGGCCAAGGGGGCGAGGTGGCGAGGTGATGGAGTATACCAC  
CATCCTCGGCTGCGCAGGGTGAATTGCCAGTGAGGGAAATATCAGTGTCATCTCCAATCACTTGGTTC  
ATCCTACTCTGCTAAAGCCAAGCTTACAGTAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACCAT  
CCGAGCTGGGGCATGGCACGCTGGAGTGTGCTGCTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA  
TGGGGGACAGACTTCCAGCTGCACGGGAGAGACGATGCATGTGATGCCGGAGGATGACGTGTTCTTATCGT  
GGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTGCAAAATGC  
AACTCTGACTGCTCTAGAAACACCATCATTTCGCGCCACTGTTGGACCGAAGTGAACCAAGGGAGAAACAGC  
CGTCTACAGTGCATTGCTGGAGGAAGGCCCTCCCCCTAAACTGAACCTGGACCAAAGATGATAGCCCATTGGTGGT  
AACCGAGAGGCACTTTGTGAGCAGGCAATCAGCTCTGATTATTGAGACTCAGATGTCAGTGCTGGAA  
ATACACATGTGAGATGCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGATCCCCACTCCAAC  
CTGCGACTCCCCCTCAGATGACAGCAGGCCACTCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGC  
CGTGGTTGCTGTGGGGCACGTCACTCGTGTGGGTGTCATCATATACACACAAAGGGGGAGGAATGAAGA  
TTGAGCATTACCAACACAGATGAGACCAACTTGCAGCAGAGTATTCTAGTTATTGTCATCTCAGGGAACGTT  
AGCTGACAGGCAGGATGGTAGCTCTCAGAAAGTGAAGGCCACCCAGTTGTCACATCTCAGGTGCTGG  
ATTTTCTTACACAAACATGACAGTAGTGGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAGCTGC  
CACAGATCTGTTCTTGTCCGTTTGGGATCCACAGGCCCTATGTTATTGAGGGAAATGTGATGGCTCAGA  
TCCTTTGAAACATATCATACAGGTGCACTGACCCAAAGAACAGTTTAATGGACCAACTATGAGCCAGTT  
CATAAAGAAAAGGAGTGTACCCATGTTCTCATCCTCAGAAGAACCTGCGAACGGCTTCAGTAATATATC  
GTGGCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTG  
TCTAAACAAGTCTCTTTAGATTTAGTGCAAATCCAGAGGCCAGCGCTGGITGCCTCGAGTAATTCTTCTATGGG  
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCC  
AAGAGCCTTTATTGAAAGCTCATCTTCCCCAGACTTGGACTCTGGGTAGAGGAAGATGGGAAAGAAAGGAC  
AGATTTCAAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAATCACAGGACTCCAAATTTCAGTC  
TTATGACTTGGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAAACATACACTCAGTGAACCTTATT  
AAAGAGAGAGAATCTTATGTTAAATGGAGTTATGAATTAAAAGGATAAAATGCTTTATTATACAGAT  
GAACCAAATACAAAAGTTATGAAAATTAACTGGGAATGATGCTCATATAAGAACACCTTTAAACTA  
TTTTTAACTTGTTTATGCAAAAAGTATCTACGTTAAATTAAATGATATAATCATGATTATTTATGTATT  
TTATAATGCCAGATTCTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCATTGACCAATT  
TTAAATAGAAGTTACTTCATTATATTGACATTATTAATAAAATGTGCAATTGAA

## **FIGURE 102**

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQLSLREVKLNNNELETIPNLGPVSAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNIRSAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMGDGFWGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAINRISPDAWE  
FCQKLSLELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLGSSLKTLDDLKNNE  
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGDALEHLDLSDNAIMSLQGNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWLPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAGQ  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTNVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPQLNWTKDDSPLVVTER  
HFFAAGNQLLIIVDSVSDAGKYTCMSNTLGERGNVRLSVIPTPTCDSQPMTAPSLEDDG  
WATVGVIIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTIAD  
RQDGYSSESSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGP  
MYLKGNVYGSDFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEESCERSFSNISW  
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS  
YDLDT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTGGTGGTGGCTGTTGGGTGCCTGCAAAATG  
AAGGATGCAGGACGCAGCTTCTCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTTAGACCCGGGGGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTTCCCCCTCC  
CCACCCCCAAAAAAAGGATGATTGGAATGAAGAACCGAGGATTACAAAGAAAAAGTATGTTCTTCTC  
TATAAAGGAGAAGTGAGCCAAGGAGATATTTGGAATGAAAAGTTGGGCTTTTAGTAAAGTAAGAAACT  
GGTGTGGTGGTGTCTTCTTCTTGAATTCCACAAGAGGGAGGAAATTAATAACATCTGCAAAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCCGAGATTGAGGCATTGATTGGGGAGAGAAACCCAGCAGAGCACAGTTGGA  
TTTGTGCCATGTTGACTAAATTGACGGATAATTGCAAGTGGATTCTCATCAACCTCCTTTTTAAAT  
TTTATTCCCTTGTATCAAGATCATGCGTTCTCTGTCTAACACCACCTGGATTTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAACAGGACAAACACCAGATAAAATTATGTAATGTTGAAACAAGAT  
GACCTTACATCCACAGCAGATAATTGAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTCT  
GCTGGCTCTCAACTCTGTGGCTGGCTGGCTCAGACCTGCCCTCTGTGTGCTCTGCCAGCAA  
CCAGTCAGCAAGGTGATTGTGTTGGAAAAACCTCGCTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT  
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAGGCACTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCAATTGAAATTGGGGCTTCAATGGTCTGGCAACCTCAACACTCTGGA  
ACTCTTGACATCGTCTTACTACCATCCGAATGGAGCTTTGTATACTTGCTCAAACGCTCTGTT  
GCGAACACAACCCATTGAAAGCATCCCTCTTATGCTTTAACAGAATTCCCTTTGCCGACTAGACTTAGG  
GGAATTGAAAAGACTTCATACATCTCAGAACGGTGCCTTGAAGGTCTGTCAAATTGAGGTATTGAAACCTTG  
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTCTGGGAAATCA  
TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACTGCCCAGAT  
TCAAGTGAACGGAATGCCTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCTCATGACCTTCACTCCCTGATCATCTAGAGCGGATACATTACATCACAAACCTTGGAACTG  
TAACTGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTGAACACAGCTTGTGCCCCGGT  
TAACACTCCTCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAATTACTTCACATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTCGGGCTCCACATC  
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCTACAAAGTGCGGATAGCTGT  
GCTCAGTGTGTTGACTGTTAACATGTAACCTGTGCAAGGATACAGGCATGTACACATGTATGGTGGTAA  
TTCCGGTGGGAAACTACTGTGTTCAGCCACCTGAAATTGTTACTGCAGCAACCAACTACTCTTCTTACTTT  
AACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGCACGGGACACAGATAACAATGTGGGCTCCACTCC  
AGTGGTCGACTGGGAGACCAATGTGACCCCTCTCACACCAACAGGACACAAGGTCGACAGAGAAAACCTT  
CACCATCCCAGTGAATGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCTGACAGACTACAAATCATCAT  
TGGGTGTTTGTGGCCATCACACTCATGGCTGCACTGATGCTGGTCAATTCTACAAGATGAGGAAGCAGCACCA  
TCGGGAAAACCATCACGCCAACAGGACTGTTGAAATTATTAAATGTGGATGAGGATTACGGGAGACACACC  
CATGGAAAGCCACCTGCCATGCCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT  
CAACCCACACAAACAGTTAACACAATAATTCAATACACAGTTCACTGCACTGACATGAGGTTATTGATCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAACAAACATCAAAAAACAA  
GACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAACAA  
AAAAGAAAAGAAATTATTAAACATTCTATTGTGATCTAAAGCAGACAAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNC  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE  
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVNSVGN  
TTASATLNVTAATTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTVEIINVDDETGDTPMESHLPMPAIEHEHLNHYN SYKSPFNHTTVNTINSIHSS  
VHEPLLIRMN SKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

## FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTCAGTTGCAGTTGGCAGTTCTTCCGTTCTGCTGTTGGGGCA  
TGAAAGGGCTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCGCACCGCACCGC  
GAGGGCGGGCGTGCACCCCTCGGCTGGAAGTTGTGCCCCGGCCCGAGCGCGCCGGCTGGAGCTTCGGTAGA  
GACCTAGGCCCTGGACCGCGATGAGCGCGAGCCTCCGTGCGCGCCGGCTGGAGCTTCGGTAGCGCTGTGC  
GCGGTGCTGGGGCGCTGGCGCTGGACAGCGGGCGTGCAGGGAACTCGGGCAGCCCTCTGGGTAGCGCC  
GAGCGCCCATGCCCACTACCTGCGCTGCCCTCGGGACCTGCTGGACTGCACTGTAAGCGGCTAGCGCTCTT  
CCCAGGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTTCC  
ATGAGCCACCTTCAAAGCTTCGAGAACAGTGAACAACAGATTGAGACCAATTCCAATCTGGGACCA  
GTCTCGGCAAAATATTACACTTCTCTTGGCTGAAACAGGATTGTGAAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTTGAACACTTGGACCTTAGCAGCAACAAATATTTCAGAGCTCAAACATGCAATTCCAGCCCTACAG  
CTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGAAACCTGGGTTTGAACATTGGCCAACACAA  
CTCCTGTGTTAAAGCTAACAGGAACCGAACATCTCAGCTATCCCACCCAAGATGTTAAACTGCCCCACTGCAA  
CATCTCGAATTGAAACCGAACAGATTAAAATGTAGATGGACTGACATTCCAAGGCTTGGTGTCTGAAGTCT  
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGACTTTTGGGGCTGAGCAACATGGAAATTG  
CAGCTGGACCATAACAAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTGCTGATGCTGAGGAACCTCAT  
CTCAGCCAAATGCCATCACAGGATCAGCCCTGATGCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA  
ACTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTGGCTAAGCTTACTAAATACACTGCACATTGGG  
AACAAACAGAGTCAGCTACATTGCTGATTGTGCCCTTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAGAAC  
AATGAAATTCTCTGGACTATTGAAGACATGAATGGTCTTCTCTGGGCTGACAAACTGAGGCAGCTGATAACTC  
CAAGGAAATCGGATCGTTCTATTACTAAAAAAAGCCTTCACTGGTTGGATGCAATTGGAGCATAGACCTGAGT  
GACAACGCAATCATGTCTTACAAGGCAATGCAATTTCACAAATGAAGAAACTGCAACAAATTGCAATTAAATACA  
TCAAGCTTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAATTTCAGAGCTTGT  
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAGGAAGAACGATTGGTGTAGCCAGATGGCTTGT  
GATGATTTCACCAAAACCCAGATCACGGTCTAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTGAGTTTC  
ATCTGCTCAGCTGCCAGCAGCTGATTCCCAATGACTTTGCTGGAAAAAAAGACAATGAACACTGCTGATGAT  
GCTGAAATGAAAATTATGCACACCTCCGGGGCCAAGGTGGCGAGGTGATGGAGTATACCACCATCCTCGGCTG  
CGCGAGGTGGAATTGCAACCTCCGGGGCCAAGGTGGCGAGGTGATGGAGTATACCACCATCCTCGGCTG  
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACCACCGAGCTGGGCC  
ATGGCACGCTGGAGTGTCTGCTGCTGGGCCACCCAGCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC  
TTCCAGCTCACGGAGAGACGCATGCTGATGCCAGGATGACGTGTTCTTATCGGGATGTGAAGATA  
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAAGTATTCAAGCAATGCAACTTGACTGTC  
CTAGAAACACCATCATTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGCTCTACAGTGC  
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCATTGGTGGTAACCGAGAGGCAC  
TTTTTGCAGCAGGCAATCAGCTCTGATTATTGAGCTCAGATGTCAGTGCTGGAAATACACATGTGAG  
ATGCTTAACACCTTGGACTGAGAGAGGAAACGTCGCCCTCAGTGTGATCCCCACTCCAACCTGCACTCCCT  
CAGATGACAGCCCCATGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGGTTGCTGT  
GTGGGGCACGTCACTCGTGTGGGTGTCATCATACACACACAAGGGAGGAATGAAGATTGAGCATTAC  
AACACAGATGAGACCAACTGCCAGATATTCTCTAGTTATTGTCATCTCAGGGAACGTTAGCTGACAGGCAG  
GATGGTACGTGCTTCAAGAAAGTGGAAAGCCACCAAGTTGTACATCTCAGGTGCTGGATTTCCTTACCA  
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGAGCTGCCACAGATCTGTC  
CTTGTGCTGTTTGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGTATGGCTCAGATCCTTGAACAA  
TATCATACAGGGTGCAGTCTGACCCAAGAACAGTTAAATGGACCACTATGAGCCAGTTACATAAAGAAAAG  
GAGTGTACCCATGTTCTCATCTTCAAGAACAGTCTGCAAGAACAGCTGGAGCTTCAGTAATATATCGTGGCTTACAT  
GTGAGGAAGCTACTTAACACTAGTTACTCTCACATGAAGGACCTGGAAATGAAAATCTGTGCTAAACAAGTCC  
TCTTAGATTGCAATCCAGAGCCAGCGCTGGTCTCGAGTAATTCTTCTATGGTACCTTGGAAAA  
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTAT  
TTGAAAGCTCATTCTCCCCAGACTTGGACTCTGGTCAAGAGGAAGATGGGAAAGAACAGATTTCAGGAA  
GAAAATCACATTGTACCTTAAACAGACTTAGAAAACACTACAGGACTCCAATTTCAGTCTTATGACTTGGAC  
ACATAGACTGAATGAGACCAAGGAAAGCTTAACATACTACCTCAAGTGAACATTATTTAAAGAGAGAAT  
CTTATGTTTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTATTATACAGATGAACCAAATTAC  
AAAAGTTATGAAAATTAACTGGGAATGATGCTCATATAAGAACACCTTTAAACTATTTTAACTT  
TTTATGAAAAAAAGTATCTACGTAATTAAATGATATAATCATGATTATTATGTTATTTATAATGCCAGA  
TTCTTTTATGGAAAATGAGTTACTAAAGCATTTAAATAACCTGCCCTGTACCATTTTAAATAGAAGTT  
ACTTCATTATATTGACATTATTTAATAAAATGTGCAATTGAAAAAAAAAAAAAA

## **FIGURE 106**

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPMSGVAAERPCPTTCRCLGDLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSF IKASSMSHLQLSREVKLNNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRI SAIPPKMFKL PQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR  
NGVTKLMGAFWGLSNMEI LQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLGSSLKTLDLKNEIS  
WTIEDMNGAFSGLDKLRRRI LQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQLHLNTSSLCDCQLKWLPQWVAENNQSFVNASCAPHQPLLKGRSIFAVSPDGVCDDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAKKDNELLHDAEMENYAHLRAQGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCAQNSA  
GSISANATLTVLETPSFLRPLLDRTVKGETAVLQCIAGGSPPPKNWTKDDSPLVVTERHF  
FAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLLDDGWA  
TVGVVIIAVVCCVVGTSLVWWVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLADRO  
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFCPFLGSTGPMY  
LKGNVYGSDFETYHTGSPDPRTVLMHYEPSYIKKKECYPCHPSEESCERSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## FIGURE 107

CAAAACTTGCCTCGCGGAGACGCCAGCTGACTGAATGGAAGGGCCCGAGCCCGGAGCGCAGCTGAGAC  
TGGGGGAGCGCTTCGGCCTGTGGGGCGCCCTGGCGCCGGGCGCAGCAGGGAAAGGGGAAGCTGTGGTCTGC  
CTGCTCCACGAGGCGCCACTGGTGTGAACCAGGGAGAGCCCCCTGGGTGGTCCCCTATCCCTCTTTATATA  
GAAACCTTCCACACTGGGAAGGCAGGGCAGGAGGGCTCATGGTGAGCAAGGAGGGCGCTGATCTGCAGG  
GCGCACAGCATTCCGAGTTACAGATTTACAGATAACCAATGGAAGGCAGGAGGCAGAACAGCCCTGCCTGGT  
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGCCGGTCTGC  
TGCTCTGCTGCTGCTGCCACAGCTGCACCTGGACCTGTGCTTGCGTGGAGGGCCCAGGATTGGCGAA  
GTGGCGCCACAGCTGAGCCCCGAAGAGAACGAATTGCGGAGGAGGAGCCGGTCTGGTACTGAGCCCTGAGG  
AGCCCCGGGCTGGCCAGCCCGTCACTGCCCCGAGACTGTGCCTGTTCCAGGAGGGCGTGTGGACTGTG  
GCGGTATTGACCTGCGTGAGTTCCGGGGACCTGCCTGAGCACACCAACCACCTATCTGCAGAACAAACCAGC  
TGGAAAAGATCTACCCCTGAGGAGCTCTCCGGCTGCACCGCTGGAGACACTGAACCTGCAAAACAAACCCTG  
CTTCCCGAGGGCTCCAGAGAAGGCAGTTGAGCATCTGACCAACCTCAATTACCTGACTTGGCAATAACAAGC  
TGACCTTGGCACCCCGTCTCTGCCAACGCCCTGATCAGTGTGGACTTGTGCTGCCAACTATCTCACCAAGATCT  
ATGGGCTCACCTTGGCCAAGGCCAAACTTGAGGTCTGTGTACCTGCACAAACAAGCTGGCAGACGCCGGG  
TGGCGGACAACATGTTCAACGGCTCCAGCAACCTGAGGTCTCATCTGTCAGCAACTCTCTGCCAACGTC  
CCAAGCACCTGCCCTGCCCTGTACAAGCTGACCTCAAGAACAAAGCTGGAGAAGATCCCCCGGGG  
TCAGCCAGCTGAGCAGCTGGCGAGCTATACTGCCAGAACAAACTACCTGACTGAGGGGCTGGACAACGAG  
CCTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAAACTGTCTGGTCCAGCTGGCTG  
CGCGCAGCCTGGTGTGCTGCACCTGGAGAACAGCCATCGGAGCGTGGAGCGAATGTGCTGACCCCCATCC  
GCAGCCTGGAGTACCTGCTGTCACAGCAACCAAGCTGCCAGGAGCAGGGCATCCACCCACTGGCTTCCAGGGC  
TCAAGCGGTTGACACGGTGCACCTGTACAACAAACCGCAGCTGGAGCGCGTGGCCAGTGGCTGCTGCC  
GCACCCCTCATGATCTGCACAAACAGATCACAGGCACTGGCGGAAGACTTGGCACCACCTACTTCTGGAGG  
AGCTCAACCTCAGCTACAACCGCATCACCAGCCACAGGGTGCACCGCGACGCCCTCCGCAAGCTGCCCTG  
GCTCGCTGGACCTGTGGGAACCCGGCTGCACACGCTGCCACCTGGGCTGCCCGAAATGTCCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCCTGGCACAGGGGCGTGGCGGGCATGGCTCAGCTGCCAGTGTACCTCA  
CCAGCAACCGACTGCCAGCCAGGCCCTGGGCCCCCTGCTGGTGGACCTGCCCATCTGCAGCTGCTGGACA  
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGCTCCCCGAGTCACCTGAGTACCTGTACCTGAGAACAAACA  
AGATTAGTGGCTGCCGCCAATGCCCTGACTCCACGCCAACCTCAAGGGGATCTTCTCAGGTTAACAAAGC  
TGGCTGTGGCTCGTGGACAGTCCTCCGGAGGCTGAAGCACCTGCAGGTCTGGACATTGAAGGCAACT  
TAGAGTTGGTACATTCAAGGACCGTGGCCCTGGGAAGGAAAGGAGGAGGAGGAAGAGGAGGAGGAGG  
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTCTTTCTGC  
AGCACACGCCCTGTGTGCTGTGAGCCCCCAACTCTGCCGTGTCACACAGAACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACCGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGTCCCAGGCCAGACACATGC  
ACACACATCACACCCCTCAAACACCCAGCTCACAGAACACAAACTACCCCTCCAAACCCACCAAGTCTGTACAC  
CCCCACTACCGCTGCCACGCCCTGTAATCATGCAGGGAGGGCTGCCCTGGCACACACAGGCCACCC  
TCCCTCCCCCTGTCAGATGTGTATGCTGACATACACACCACACACATGCACAAAGTCATGTGCGAA  
CAGCCCTCCAAAGCTATGCCACAGACAGCTTGTGCCAGGAGAACATCAGGCCATAGCAGCTGCCGTCTGCC  
GTCCCATCTGTCCGTTCCCTGGAGAAGACACAAGGGTATCCATGCTGTGGCCAGGTGCTGCCACCC  
GGAACTCACAAAAGCTGGTTTATTCTTCCATCCTATGGGACAGGAGCTTCAGGACTGCTGCCCTGG  
TGGCCACCCCTGCTCCTCCAGGTGCTGGCAGTCACCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACCTTCCAATGGGAAGGCCAGTGGAGGGCAGGATGGAGAGGCCCTGGGTGCTGCTGGGGCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT  
GTTCTTCAGGCTGTGGGGGAAGTTCCGGTGCCTTATTCTTATTCTTCTAAGGAAAAAAATGATAAAA  
CTCAAAGCTGATTCTTCTTGTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENEFAEEEPLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP  
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFEHTNLNYLYLANNK  
LTTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSDANVLPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPDRVRLMILHNQITGIGREDFATTYF  
LEELNLSYNRITSQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKIGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEETR

**Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

**Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## FIGURE 109

GGGAGGGGGCTCCGGGCCGCGCAGCAGACCTGCTCCGGCGCGCCTGCCGCTGCTCTCCGGAGCGGCAG  
CACTAGCCGGCGCGAGGGCTGGGGTCTCGAGACTCTCAGAGGGCGCCTCCATGGCCCACCA  
CAACCTGTTCTCGCGCCACTGCGCTGCCAGGACCCGCTGCCAACATGGATTTCCTGGCGTGGT  
GCTGGTATCCTCGCTCACCTGCAAGCGGCCGAGTCAGCGAGGTGGCCAGGAAATAGTGTATCGAT  
TGGCCTATGCGTTATGGGGAGGATTGACTGCTGCTGGGGCTGGCTGCCAGTCTTGGGACAGTGTAGCC  
TGTGTGCCAACCACGATGCAAACATGGTGAATGTATGGGCCAACAAAGTCAAGTGTATCCTGGTTATGCTGG  
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCCGCCCTGTAAGCACAGGTGATGAACACTTA  
CGGCAGCTACAAGTGTACTGTCTAACGGATATATGCTCATGCCGATGGTCTCTGCTCAAGTGCCCTGACTG  
CTCCATGGCAAACAGTGTAGTGGCTGTGATGGTTAAAGGACAAATACTGGGCCAGTGCCATCCCTGGCCT  
GCACCTGGCTCTGTGGAGGACCTGTGATGGTGAATGTGCTACAGGAAGAGCCTCTGCCCTAGATT  
TAGGCAATGTGTCAACACTTGGGAGCTACATCTGCAAGTGTCAAAAGGCTTCGATCTCATGTATATTGGAGG  
CAAATATCAATGTCATGACATAGACGAATGCTCACTGGTCAGTATCAGTGAGCAGCAGTGTGCTGATGTTAA  
CGTAGTGGTCTACAAGTGCACAAATGTAAGGAGGATACAGGGTGAATGGACTGACTTGTGTTATATCCAAA  
AGTTATGATTGAACCTCAGGTCCAATTGATGTTACCAAAAGGAAATGGTACCATTTAAAGGGTACACAGGAAA  
TAATAATTGGATTCCGTGATGGAGTACTGGTGGCTCCGAAGACACCATATATTCCCTATCATTACCAA  
CAGGCCTACTCTAACAGCAACAAGACCTACACCAAGCCAACACCAATTCTACTCCACCACACC  
CCTGCCAACAGAGCTCAGAACACCTTACACCACTACACCCAGAAAGGCCAACACCAGGACTGACAACATAGC  
ACCAGCTGCCAGTACACCCAGGAGGATTACAGTTGACAACAGGGTACAGACAGACACCCTGAGAAACCCAGG  
AGATGTGTTAGTGTCTGGTACACAGTTGTAATTGGACCATGGACTTTGGATGGATCAGGGAGAAAGACAA  
TGACTTGCACTGGAAACCAATCAGGGACCCAGCAGGTGACAATATCTGACAGTGTGGCAGCCAAGCCCCAGG  
GGGAAAAGCTGCACGCTGGTGTACCTCTGGCCCTCATGCATTAGGGACCTGTGCTGTGATTAGGCA  
CAAGGTGACGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTCCCCACGGAGCAGCCCTGTG  
GGGAAGAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTTGCAGGGGCTGACATCAAGAGCGAATCACA  
**AAGATGATTAAGGGTTGGAAAAAAAGATCTATGATGGAAAATTAAAGGAACACTGGATTATTGAGCCTGGAGAAG**  
AGAAGACTGAGGGCAAACCAATTGATGGTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCACCAGCTG  
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG  
GCCATTGTTAGAATACTTCATAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTCTAAATTAGA  
TAAAATTTGCTATTAAAGATGGTAAAGATGTTCTTACCAAGGAAAAGTAACAAATTATAGAATTCCAAA  
AGATGTTTGATCTACTAGTAGTATGCACTGAAAATCTTACAATTAAATTGGACAAGGCTTAATTAGG  
CATTTCCCTCTGACCTCTAAATGGAGAGGGATTGAAAGGGGAAAGAGGCCACAAATGCTGAGCTCACTGAAATA  
TCTCTCCCTTATGGCAATTCTAGCAGTATTAAGAAAAAAAGGAAACTATTCTTCAAATGAGAGTATGATGGAC  
AGATATTGTTAGTATCTCAGTATGTTCTAGTGTGGCGGTGTTCAATGTTCTCTTCAAGGTAAGGTATAAGCC  
TTTCATTGTTCAATGGATGATGTTCAAGGTTCTTAAAGAGATCCTTCAAGGAACACAGTTCAAGAG  
ATTTTCATGGGTGCATTCTCTGCTTGTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCTGCC  
ACACCGGCAGACCTTCCCTCACCTCATCAGTATGATTGATTCTCTTATCAATTGGACTCTCCAGGTTCCAC  
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTTGTCAATTAAACCTGGTAAAGGCAGGGCTGG  
AGGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTAAATGGTTATT  
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAATTTCAGTTCTGATGCCAA  
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTAATGTTT  
CTAAAATAAAATGTTAGTGGTTTCAAATGGCTAATAAAAACAATTATGTAAATAAAACACTGTTAGTAAT

FOOTER: 4298000000

## **FIGURE 110**

MDFLLALVLVSSLYLQAAAEDGWRPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP  
RCKHGE CIGPNKCKCHPGYAGKTCNCQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRC  
VNTFGSYICKCHKGFDLMIYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTTPERPTTGLTTIAPA AASTPPGGITVDN  
RVQTDPQKPRGDVFSLVHSCNFDHGLCGWIKEKDNDLHWEPIRD PAGGQYLTVSAAKAPGG  
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHS GTLQVFVRKHGAHGAALWGRNGGHGWRQTQI  
TLRGADIKSESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## **FIGURE 111**

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA  
**AATGTGGCTCAAGGTCTCACAACTTCCCTTCCTTGCAACAGGTGCTGCTCGGGCTGA**  
AGGTGACAGTGCACATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA  
ACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGAATACC  
AACACAAGTTCACCATGATGCCACCCAAATGCATCTGCTTATCAACCCACTGCAGTCCCT  
GATGAAGGCAATTACATCGTAAGGTCAACATTCAAGGAAATGGAACATCTATCGCCAGTCA  
GAAGATAACAAGTCACGGTGATGATCCTGTACAAAGCCAGTGGTGCAAGATTCACTCCCT  
CTGGGGCTGTGGAGTATGTGGGAACATGACCCGTACATGCCATGTGGAAGGGGCACTCGG  
CTAGCTTACCAATGGCTAAAAAAATGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTC  
TCCCCAAAACAATACCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAAATTACAGCT  
GCCTGGTGAGGAACCTGTCAGTGAATGGAAAGTGATATCATTATGCCCATCATATTAT  
GGACCTTATGGACTTCAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTACTGT  
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGGCCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTTACAACAAACATAAC  
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTTG  
CACAGAAAGGAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTTGATT  
ATATCCATGTGCTTCTCTTCTATGGAAAAAAATCAACCCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATGGGGCAAGATTGCACAGTACAGT  
GTATGAAGTTATTCACTGACATCCCTGCCAGCAGCAAGACCATCCAGAGT**GAAC**TTTCA  
GCTAAACAGTACATTGAGTGAATTCTGAAGAAACATTAAAGGAAAACAGTGGAAAAGT  
ATATTAATCTGGAATCACTGAAGAAACCAGGACCAACACCTCTACTCATTATTCCCTTACA  
TGCAGAATAGAGGCATTATGCAAATTGAACTGCAGGTTTCAGCATATACACAATGTCTT  
GTGCAACAGAAAAACATGTTGGGAAATATTCCCTCAGTGGAGAGTCGTTCTGCTGACGG  
GGAGAACGAAAGTGACAGGGTTCTCATAAGTTGTATGAAATATCTCTACAAACCTCA  
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA  
TGTGGAAACTTACATTGTTGATTTCAATTATTCCAAATTCTATCTTGTATTAGTG  
TTAAGAATGCTAAATTATGTTCAATTATTCCAAATTCTATCTTGTATTGTACAA  
CAAAGTAATAAGGATGGTTGTCAACAAAACAAAATATGCCCTCTCTTTTTCAATCACC  
AGTAGTATTGGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA  
TTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTGTCTTAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ  
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 113**

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGCAGTTCCCCTGGCAGTCCTGGTGTGCTGTT  
GCTTTGGGGTGCTCCCTGGACGCACGGCGGCCGGAGCAACGTTCGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTATGCCCGTGGTGCCTGCT  
TGTCAAAATCTCAACCGGAATGGAAAGTTGCTGAATGGGGAGAAGATCTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC  
TTCCTACTATTATCATTGTAAGATGGTGAATTAGGGCCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAAACTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCCCTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT  
GTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC  
AGATTGCCTTGTCCCTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAAT  
TATTATCAGAACATCTGCACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA  
GATGTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAACATGC  
CATAAAGACAACGCTCTGGTCCATCATTGGCACAGATAAACTCTAGTTAAATTATAG  
TTATCTTAATATTGATTTGATAAAACAGAACAGATTGATCATTGTTGGTTGAAGTG  
AACTGTGACTTTTGAAATATTGCAAGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA  
CATTCAAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTAAAGCACAGTATGATG  
GTTTAAATAGTTCTCTAATTGAAAAATCGTGCACAGAACATAAGATTGATATTGTTGTTG  
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGCAATT  
TGAGGTATTAAAGAAGATTATTAGAGAAAAATTACATTCTCATTGATATAATTGTTCTG  
TTCACTGTGAAAAAAAGAACATATTCCCATAAAATGGAGTTGCCATTGTCCTCAAG  
AAATGTGATTTCAGTACAATTCTGGTCTTTAGAGGTATATTCCAAATTTCCTGTT  
ATTAAATTGTTATGCAACTAAACACTACCTACATTAAATTACAGTTCTACACA  
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTCTGATT  
CAACAAAGTTGATTTCTCTGATTTCCTACTTACTATGGTTACATTGTTATT  
CAAATTGGATGATAATTCTGGAAACATTGTTATGTTAGTAAACAGTATTGTT  
GTTTCAAACACTGAAGTTACTGAGAGATCCATCAAATTGAACAATCTGTTGAATT  
TTGGCCACTTTTCAGATTACATCATTGCTGAACATTCAACTGAAATTGTT  
TTCTTTGGATGTAAGGTGAACATTCTGATTGTTCTGATGTGAAAAAGCCTGGTA  
TTTACATTGAAAATTCAAAGAAGCTTAATATAAAAGTTGCTACTCAGGAAAAAG  
CATCTCTTGATATGCTTAAATGTATTGTTCTCATACAGAAAGTTCTAATTGAT  
TTTACAGTCTGTAATGCTGATGTTAAAATAAAACATTGTTATT  
ACTTCATATTATCCTGTGTTCTTCCTGACTGGTAATATTGTTGTTGGATT  
GTCAGTAGGATGGAACATTAGTGTATTGTTACTCCTAAAGAGCTAGAATACATAGTT  
CACCTTAAAAGAAGGGGAAAATCAAATACAATGAACACTGACCAATTACGTAGTAGAC  
AATTCTGTAATGTCCTCTTCTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG  
TATCGTAATATAACAGTTCTTAAAGCCCTCTCCTTAAAGAGCTAGAATACATAGTT  
AAAGAGTTGGATGTTGTAACCTGATGCCTTAAAGAAAAATATCCTAAGCACAAAATAACCT  
TTCTAACCACTCATTAAAGCTGAAAAAAAAAAAAAA

## FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## **FIGURE 115**

GCGAGTGTCCAGCTCGGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGC GGATTGGAAGAGCGGG  
AAGGT CCTGGCCCAGAGCAGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC  
ATTGCTGATGGCTGGTTGGTGTCTGAGCTGTGCAGGCCAATTCTCACCTCTATTG  
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCCCTGCAGGACTCAGCTGCA  
GGTTTATCGCCAACCTCTGTGCAGCGGAGTTCTCCCCACTGATGAGGAGGAGATAGG  
AGCTGCCAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA  
GAGGGGAACTTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG  
GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGTGATGCCGGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGCTCACCCGCCCTGCTC  
TCCCTTGACCCAAAGCCACGAACGAGCTGGAGGGAAATCTGCGGTACTTGTAGCAGTTATTGGA  
GGAAGAGAGAGAAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGGCA  
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTGTGCGGG  
GAGGGTGTCAAACGTACGACACCCGTAGACAGAAGAGGGCTTCTGTAGGTACCAACATGGCAA  
CAGGGCCCCACAGCTGCTCATTGCCCTTCAAAGAGGAGGACGGAGTGGACAGCCCGCACA  
TCGTCAGGTACTACGATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA  
CCTAAACTTGCACGCCACCGTGTGATCCAAGACAGGAGTCTCACTGTGCCAGCTA  
CCGGGTTTCCAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGGCCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT  
TATGGAGTGGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGGCACCTTTGACAGCGG  
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACTACATGAGTGTAGAAGCTG  
GTGGTGCCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG  
TTCTGGTACAACCTCTGCGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCTGCC  
TGTGCTTGTGGCTGCAAGTGGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTCTGTCCCTCCCTGGTC  
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT  
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCCAGCCCTCCATTCAAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA  
AAGTGGCTGAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTCAGTGAACCAAAGTTCTGATACCTGTTACATGTTGTTTAT  
GGCATTCTATCTATTGTGGCTTACCAAAAATAAAATGCCCCAACAGAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR  
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVVDYLPERDVYESLCRGEVKLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMDSDEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKGTAVFWYNLLRSGEDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEV

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## FIGURE 117

GCAGTATTGAGTTTACTCCTCTTTTAGTGGAAAGACAGACATAATCCCAGTGTGAGTGAAATTGATTGT  
TTCATTTATTACCGTTGGCTGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA  
AGACAGGACAATCTCTGGGGATGCTGGTCCTGGAAGGCCAGCGGGCCTGCTCTGCTTTGGCCTCATTGACCC  
CAGGTTCTCTGGTTAAACTGAAAGCCTACTACTGGCCTGGTGCCATCAATCCATTGATCCTTGAGGCTGTGCC  
CCTGGGGCACCCACCTGGCAGGGCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGCTTC  
CCCTCATCTTAGGGCTGCTCTGGGGTGCAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG  
ATCCCTGTGTCGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG  
ATGAAGACTTCAAACCCCGATTGCCCCACTACAGGGACCCACAAGCCTACAAGAAGGTGTCAGGAAC  
GGTACATCCAGACAGAGCTGGCTCCGTGAGCGGTTGCTGGTGGCTGACCTCCGAGCTACACTGTCCA  
CTTTGGCCGTGGCTGTGAAACCGTACGGTGGCCATCACTTCCCTCGGTTACTCTACTTCACTGGCAGCGGGGG  
CCCGGGCTCCAGCAGGGATGCAAGTGGTGTCTCATGGGATGAGCGGCCGCTGGCTATGTCAGAGACCCCTGC  
GCCACCTTCACACACACTTGGGGCCACTACGACTGGTCTTCATCATGCAAGGATGACACATATGTGCAAGGCC  
CCCGCTGGCAGCCCTGCTGGCCACCTCAGCATCAACCAAGACCTGACTTAGGCCGGCAGAGGAGTTATTG  
GCGCAGGCGAGCAGGCCGGTACTGTCATGGGGCTTGGCTACCTGTTGTCACGGAGTCTCCTGCTTCGTC  
GGCCACATCTGGATGGCTGCCAGGGAGACATTCTCAGTGGCTCTGACGAGTGGCTTGGACGCTGCCATTG  
ACTCTCTGGGCGTCGGCTGTGTCACAGCAGGGCAGCAGTATGCTCATTTGAATGGCCAAAATAGGG  
ACCTGAGAAGGAAGGGAGCTCGGCTTCTGAGTCGCTGCCACCTGCTCCGAAGGTACCCCTCATGT  
ACCGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTAAATAGAACAACTGCAAGCTCAGA  
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA  
CACACACACTCTGCTTGTAGGTGCTGGACTACTTCACAGAGCAGCACACCTCTCTGCAAGATGGG  
CTCCAAGTGCCTACTACAGGGGCTAGCAGGGCGACGTGGTGTGCTGGAGACTGCCCTGAGCAGCTCA  
ATCGCGCTATCAGCCCCGCTGCGCTTCCAGAAGCAGCGACTGCTCAACGGTATCGCGCTTCGACCCAGCAC  
GGGCATGGAGTACACCTGGACCTGCTTGGAAATGTTGACACAGCGTGGCACCAGGGGGCCCTGGCTCGCA  
GGTCAGCCTGCTGCCACTGAGCCGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCGAGTGC  
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGAGCCCCGGCTTCTGAGGCGTTGAGCCAATGTCC  
TGGAGCCAGAGAACATGCTCACCCTGTTGCTGGTCTACGGGCCACGAGAAGTGGCCGGAGCTCCAG  
ACCCATTCTGGGTGAAGGCTGAGCAGGGAGTTAGAGCAGGGTACCTGGACGAGGCTGGCTGGCTCG  
CTGTGCGAGCAGAGGCCCTCCAGGTGCGACTCATGGACGTGGCTCGAAGAAGCACCTGTGGACACTCTCT  
TCTTCTTACCAACCGTGTGGACAAGGCTGGCCGAAGTCTCAACCGCTGCGATGAATGCCATCTGCT  
GGCAGGCCCTTCCAGTCCATTCCAGGAGTTCAATCTGCCCTGTCACCACAGAGATCACCCCCAGGGCCCC  
CGGGGCTGGCCCTGACCCCCCCTCCCTGGTGTGACCCCTCCGGGGGCTCTATAGGGGGAGATTG  
ACCGGCAGGCTCTGCGGAGGGCTGCTTCTACAACGCTGACTACCTGGCCGCCAGGCCGGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGGAGGAAGGCCCTGGAGGGCTGGAGGGTGTGGATGTTCTCCGGTTCTCAGGGCTCC  
ACCTTTGGGGCGTAGAGGCCAGGGCTGGTGTGAGAAGTTCTCCCTGCGAGACTGAGGCCACGGCTCAGTGAAG  
AACTCTACCACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGCCGTGCCAGCTGGCTATGGCTCTTTG  
AGCAGGAGCAGCCAATAGCACTTAGCCCGCTGGGGCCCTAACCTATTACCTTGTCTGCCAGCC  
CCAGGAAGGGCAAGGAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA  
ACATGTCTTGTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD  
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV  
AHHPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSRLLLRLPHLDGCRG  
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPNSRFEV  
LGWDYFTEQHTFSCADGAPKCPLOQASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR  
RFDPARGMEYTLDLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPPLL  
VAEAAAAPAFLEAFAAVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAEEEELERRYPG  
TRLAWLAVRAEAPSQVRLMDVSVSKHPVDTLFFLTTWTRPGPEVLRCRMNAISGWQAFFP  
VHFQEFPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA  
RARLAGELAGQEEEALEGLEVMDFVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRQLAMALFEQEQANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## FIGURE 119

CGGAGTGGTGCACGTGAGAGGAAACCGTGCACGGCTGCCTTCCTGTCCCCAAGCC  
GTTCTAGACGCCGGAAAAATGCTTCTGAAAGCAGCTCTTTGAAGGGTGTGATGCTTGG  
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC  
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG  
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTAAATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAAC  
GTTCTCCTGCACGCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAAGAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAATACCAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC  
CAACCAGGTAGTAGAAGGCTGTTGTCAGATATGGCTTACTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGTATGGGTATACCGCCTAGGGCATTGGCATATTTCAAT  
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTGTATAGGACGTGTGTCATTATTGTAGTAGTAACATATCCAA  
TACAGCTGTATGTTCTTTCTTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGAAATG  
TGTTGGAAAGAAGTGTAAAGAATAATAATTGCAAATAAACTATTAAATAATATTAT  
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT  
AAAAAAATTAAACAGGTCTTAGCGTTCAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAACTTTAGCTGTGTGTTCCCTTACTTCTAATACGTATTATGTTCT  
AAGCCTCCCCAAGTTCCAATGGATTTGCCTCTCAAATGTACAACTAAGCAACTAAAGAAA  
ATTAAAGTGAAAGTTGAAAAT

## FIGURE 120

MLSSESSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNMDWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIENLYFLLKKDPSPQFYLGHTIKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 121**

## **FIGURE 122**

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDATMRDSS  
NPRQNWNNDVTCFLNYFRICEMVGINPLNKGKSL

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## FIGURE 123

GGGACTACAAGCCGCGCGCTGCCGCTGGCCCCCTCAGCAACCCCTGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGGCCTCGGCTGCTGACTTCTTCCTGCTGCTGCTTTCTAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTTGATCATTACGGATTGCG  
AGACAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGCTCGTGCAGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTATCGCTGTGAGGTCGTTGCTGAAATGACCGCAAGGAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGCTGTAGAGTGGCAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGAATGATGTACCAACTGCCACGGATT  
CCAGAGCCAATCCCAGATTGCAATTCTTCCACTTAAACTCTGAAACAGGACTTTGGTGTCACTGCTG  
TTCACAAGGACACTCTGGCAGTACTACTGCATTGCTTCCAATGACGCAAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTTCTGGTTGCTCTTGCTGTACTGGCCCTGA  
TCACGTTGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGAAACCAAGATGGAGTTAACTACATCCGCACTGACGAGGGGCACTTCAGACACAAGTCATGTTTG  
TGATCTGAGACCCGCGGTGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGCTAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAAGGCTTTGCTTGGCCAAAGTTGACCA  
CTACTCTTCACTCTAACACGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAATATAACCAA  
GGAAAGGAAACTGGGTGCGTTCACTGAGTTGGGTTCTAATCTGTTCTGGCTGATTCGGCCATGAGTTAGG  
GTGATCTTAAAGAGTTGCTCACGTAACAGCCCCTGAGGCTGGACAGCACCAGCAGCGCATCCGGGGAAACCA  
GAAAAGGCTTCTACACAGCAGCCTTACTTCATCGGCCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCACTGCTTCACTGAGGCTGGGATCAGCAGGTTGTTCAAGGCTTAAAGGCTCTGC  
GTAAATTGGTTGCTGGAAGAGGGATCTTGCTGAGGAACCCCTGCTGCTTCAACAGGGTGTCAAGGATTTAAGGAAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTGTTATTATAAAATT  
TACATCTAAATTGGTCAAGGATGTATTGATTATTGAAAAGAAAATTCTATTTAAACTGTAATATATTGT  
CATACAATGTTAAATAACCTATTGGTAAAGGCTTCAACTTAAGGTTAGAAGTCTAACGCTACTAGTGTAAAT  
TGGAAAATATCAATAATTAGAGTTGGGTTACCAAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTCT  
CACACAAGTTTACGCTTTTACAAGGAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAATTCCAGTTAACGAAATGTTGAAATCAGTTGCTCTCTTCAAAAGAAACCTCTCAGGTTAGCTTGA  
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCTCAGATGTACATACAGATG  
CCAGTCAGCTCTGGGTTGCGCCAGGCGCCCCGCTCTAGCTACTGTCCTGCTGCTGCCAGGAGGCCCT  
GCCATCCTGGCCCTGGCAGTGGCTGTGCTCCAGTGAGCTTACTCACGTGCCCTTGCTCATCCAGCACAGC  
TCTCAGGTGGCACTGCAGGGACACTGGTGTCTTCCATGCTAGCGTCCCAGCTTGGCTCTGTAACAGACCTCT  
TTTGGTTATGGATGGCTCACAAATAGGGCCCCCAATGCTATTGGTTAAAGTTGTTAATTATTGTT  
AAGATTGCTAACGGCAAAGGAAATGCGAAATCAAGTCTGTCAGTACAATAACATTGTTAAAGAAAATGGAT  
CCCACTGTTCTTGGCTTGCACAGAGAAAGCACCAGCCAGGCTCTGCTGCTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCTGGGGAGGAAAG  
TGAAAAGCCTGAATCAAAGCAGTTCTAATTGACTTTCAATTGGTACATCCGCGGAGACACTGCTCCATT  
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GCCGTGCTGGACTCAGGACTGAAGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGCTGG  
GAATGGCTCTCACTACTCACCTGCTTCACTGCTTCAAGGCTCTGCTTGGTTTTTATACATTGACAGCTTTTTT  
AATTGCTACATGAGACTGTGTTGACTTTTTAGTTATGAAACACTTGGCGCAGGCCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGATGGCATCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTACCGCTCCAGCCTCCT  
TCTTGGTTGTCAGTGATAGGGTAGCCTTATTGCCCCCTTCTTACACCTTACACTAGTGCA  
TGGGAAACCAGGCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCTTACACTGAGACTAGA  
CGGAAAAGGAATACTGTTGATTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
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## **FIGURE 124**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRRLCARLPDFFLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSFVI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267